

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 5, 2004, 15:24:02 ; Search time 17 Seconds
(without alignments)
1537.601 Million cell updates/sec

Title: US-09-703-951A-12
Perfect score: 2702
Sequence: 1 MRCSPGGVWLALASLLHVS.....TIGILMSAPNFVEAVSKDFA 502

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2702	100.0	502	1 ACH7 HUMAN	P36544 homo sapien
2	2549	94.3	502	1 ACH7 MOUSE	P49582 mus musculu
3	2540	94.0	499	1 ACH7 BOVIN	P54131 bos taurus
4	2535	93.8	502	1 ACH7 RAT	Q05941 rattus norv
5	2433	90.0	502	1 ACH7 CHICK	P22770 gallus gall
6	1108.5	41.0	498	1 ACH1 CAEEL	P48180 caenorhabdi
7	964.5	35.7	516	1 ACH1 MANSE	P91766 manduca sex
8	949	35.1	529	1 ACH2 HUMAN	Q15822 homo sapien
9	949	35.1	557	1 ACH1 SCHGR	P23414 schistocerc
10	944.5	35.0	511	1 ACH2 RAT	P12389 rattus norv
11	942.5	34.9	459	1 ACHN CARAU	P19370 carassius a
12	941.5	34.8	528	1 ACH2 CHICK	P09480 gallus gall
13	938	34.7	622	1 ACH4 CHICK	P09482 gallus gall
14	937.5	34.7	576	1 ACH2 DROME	P17644 drosophila
15	936	34.6	503	1 ACH3 HUMAN	P32297 homo sapien
16	926	34.3	496	1 ACH3 CHICK	P09481 gallus gall
17	926	34.3	567	1 ACH1 DROME	P09478 drosophila
18	923	34.2	629	1 ACH4 MOUSE	O70174 mus musculu
19	920	34.0	627	1 ACH4 HUMAN	P43681 homo sapien
20	919.5	34.0	495	1 ACH3 BOVIN	Q07263 bos taurus
21	914	33.8	495	1 ACHP RAT	P12392 rattus norv
22	912	33.8	630	1 ACH4 RAT	P09483 rattus norv
23	905.5	33.5	499	1 ACH3 RAT	P04757 rattus norv
24	898	32.9	494	1 ACH6 CHICK	P49581 gallus gall
25	885	32.8	498	1 ACHP HUMAN	P30926 homo sapien
26	882	32.6	521	1 ACH3 DROME	P04755 drosophila
27	880.5	32.6	491	1 ACHN CHICK	P09484 gallus gall
28	880	32.6	470	1 ACHP CHICK	P26153 gallus gall
29	878	32.5	512	1 ACH3 CARAU	P18845 carassius a
30	871.5	32.3	450	1 ACHX HUMAN	Q9GZ26 homo sapien
31	871.5	32.3	494	1 ACH6 HUMAN	Q15825 homo sapien
32	866.5	32.1	493	1 ACH6 RAT	P43143 rattus norv
33	865	32.0	502	1 ACHN HUMAN	P17787 homo sapien

RESULT 1

ACH7_HUMAN	STANDARD;	PRT;	502 AA.
ID	ACH7_HUMAN	STANDARD;	PRT; 502 AA.
AC	P36544; Q15826; Q96RH2; Q99555; Q9BXH0;		
DT	01-JUN-1994 (Rel. 23, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	Neuronal acetylcholine receptor protein, alpha-7 chain precursor.		
GN	CHRNA7 OR NACHRA7.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
EX	MEDLINE=94195283; PubMed=8145738;		
RA	Peng X., Katz M., Gerzanich V., Anand R., Lindstrom J.;		
RT	"Human alpha 7 acetylcholine receptor: cloning of the alpha 7 subunit from the SH-SY5Y cell line and determination of pharmacological properties of native receptors and functional alpha 7 homomers expressed in Xenopus oocytes.";		
RT	Mol. Pharmacol. 45:546-554(1994).		
RL	[2]		
RN	SEQUENCE FROM N.A.		
RP	TISSUE=Hippocampus;		
RC	Logel J., Drebing C., Barnhart M., Antle C., Leonard S.;		
RA	Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.		
RL	[3]		
RN	SEQUENCE FROM N.A.		
RP	MEDLINE=97062879; PubMed=8906617;		
RA	Elliot K.J., Ellis S.B., Berckhan K.J., Urrutia A.,		
RT	Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.;		
RT	"Comparative structure of human neuronal alpha 2-alpha 7 and beta 2-beta 4 nicotinic acetylcholine receptor subunits and functional expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and beta 4 subunits.";		
RT	J. Mol. Neurosci. 7:217-228(1996).		
RL	[4]		
RN	SEQUENCE FROM N.A.		
RP	MEDLINE=97162233; PubMed=9009220;		
RA	Groot Kormelink P.J., Luyten W.H.M.L.;		
RT	"Cloning and sequence of full-length cDNAs encoding the human neuronal nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and expression of seven nAChR subunits in the human neuroblastoma cell line SH-SY5Y and/or IMR-32.";		
RT	FEBS Lett. 400:309-314(1997).		
RL	[5]		
RN	REVISIONS.		
RP	Groot Kormelink P.J., Luyten W.H.M.L.;		
RA	Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.		
RL	[6]		
RN	SEQUENCE FROM N.A.		
RP	TISSUE=Epidermal keratinocytes;		
RC	Arredondo J., Grando S.A.;		
RA	"Cloning cholinergic receptors in human keratinocytes.";		
RT			

P25108 rattus norv
Q9ugm1 homo sapien
P04756 mus musculu
Q23022 caenorhabdi
P02709 bos taurus
P45963 caenorhabdi
P25162 drosophila
P09479 gallus gall
P12390 rattus norv
P43144 rattus norv
Q98880 brachydanio
P22456 xenopus lae

ALIGNMENTS

Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 [7]
 RN SEQUENCE OF 17-502 FROM N.A.
 RC TISSUE=Brain;
 RA Doucette-Stamm L., Monteggia L.M., Donnelly-Roberts D., Wang M.T.,
 RA Lee J., Tian J., Giordano T.;
 RT "Cloning and sequence of the human $\alpha 7$ nicotinic acetylcholine
 RT receptor";
 RL Drug Dev. Res. 30:252-256 (1993).
 RN [8]
 RN SEQUENCE OF 24-502 FROM N.A.
 RP TISSUE=Retina;
 RX MEDLINE=94245214; PubMed=8188270;
 RA Chini B., Raimondi E., Elgoyhen A.B., Moralli D., Balzaretto M.,
 RA Heinemann S.F.;
 RT "Molecular cloning and chromosomal localization of the human $\alpha 7$ -
 RT nicotinic receptor subunit gene (CHRNA7).";
 RL Genomics 19:379-381 (1994).
 RN [9]
 RN SEQUENCE OF 118-129 FROM N.A.
 RP MEDLINE=21818878; PubMed=11829490;
 RA Riley B., Williamson M., Collier D., Wilkie H., Makoff A.;
 RT "A 3-Mb map of a large segmental duplication overlapping the $\alpha 7$ -
 RT nicotinic acetylcholine receptor gene (CHRNA7) at human 15q13-q14";
 RL Genomics 79:197-209 (2002).
 RN [10]
 RN MASS SPECTROMETRY.
 RC TISSUE=Breast cancer;
 RX MEDLINE=21829512; PubMed=11840567;
 RA Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A.,
 RA Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J.,
 RA Zvelebil M.J.;
 RT "Cluster analysis of an extensive human breast cancer cell line
 RT protein expression map database";
 RL Proteomics 2:212-223 (2002).
 CC -!- FUNCTION: After binding acetylcholine, the AChR responds by an
 CC extensive change in conformation that affects all subunits and
 CC leads to opening of an ion-conducting channel across the plasma
 CC membrane.
 CC -!- SUBUNIT: Forms a homo-oligomeric channel blocked by alpha-
 CC bungarotoxin. The structure is probably pentameric (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- MASS SPECTROMETRY: MW=54157.68; METHOD=MALDI.
 CC -!- SIMILARITY: Belongs to the ligand-gated ionic channel family.
 CC -----
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 CC -----
 DR EMBL; X70297; CAA49778.1; -;
 DR EMBL; U40583; AAB3561.1; -;
 DR EMBL; U62436; AAB40114.1; -;
 DR EMBL; Y08420; CAA69697.1; -;
 DR EMBL; AF385585; AAK68111.1; -;
 DR EMBL; L25827; -; NOT ANNOTATED CDS.
 DR EMBL; Z23141; CAA80672.1; -;
 DR EMBL; AF332758; AAK19515.1; -;
 DR PIR; G02259; G02259.
 DR PIR; I37185; ACHUA7.
 DR Genew; HGNC:1960; CHRNA7.
 DR MIM; 118511; -;
 DR GO; GO:000582; C:nicotinic acetylcholine-gated receptor-chan. .; TAS.
 DR GO; GO:0015464; F:acetylcholine receptor activity; TAS.
 DR GO; GO:0004889; F:nicotinic acetylcholine-activated cation-se. .; TAS.
 DR GO; GO:0000187; P:activation of MAPK; TAS.
 DR GO; GO:0006810; P:transport; TAS.
 DR InterPro; IPR006029; Neu_chan_memb.
 DR InterPro; IPR006202; Neu_chan_LBD.

InterPro; IPR006201; Neur_chanel.
 DR Pfam; PF02931; Neur_chan_LBD; 1
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMS; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
 DR Postsynaptic membrane; Ionic Channel; Glycoprotein; Signal;
 KW Transmembrane; Multigene family.
 FT SIGNAL 1 22
 FT CHAIN 23 502
 FT BY SIMILARITY
 FT NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
 FT ALPHA-7 CHAIN.
 FT EXTRACELLULAR (POTENTIAL).
 FT POTENTIAL.
 FT POTENTIAL.
 FT POTENTIAL.
 FT CYTOPLASMIC (POTENTIAL).
 FT POTENTIAL.
 FT BY SIMILARITY.
 FT ASSOCIATED WITH RECEPTOR ACTIVATION
 FT (BY SIMILARITY).
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT A -> G (IN REF. 1 AND 7).
 FT S -> N (IN REF. 2 AND 6).
 FT S -> P (IN REF. 2 AND 6).
 FT C -> S (IN REF. 8).
 FT A -> G (IN REF. 1).
 FT RMACS -> AWPAP (IN REF. 8).
 FT D94B3A482EAA0E42 CRC64;
 SQ SEQUENCE 502 AA; 56449 MW; 56449 MW;
 Query Match 100.0%; Score 2702; DB 1; Length 502;
 Best Local Similarity 100.0%; Pred. No. 9,6e-213;
 Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MRCPGQGVWALAAALHVSLSQGEFQKLYKELVKNVPLRPVANDSQELTVYFSL 60
 Db 1 MRCPGQGVWALAAALHVSLSQGEFQKLYKELVKNVPLRPVANDSQELTVYFSL 60
 Qy 61 QIMDVDEKNOVLTNTIWLQSWTDHYLQWNVSEYGVKTVRFPDQGLWKPDILLYNSADE 120
 Db 61 QIMDVDEKNOVLTNTIWLQSWTDHYLQWNVSEYGVKTVRFPDQGLWKPDILLYNSADE 120
 Qy 121 RFDATEFTNVLVNSSGHGHCQLPPGIPKSSCYIDVRWFPFDVQHCKLFGSWSYGSW 180
 Db 121 RFDATEFTNVLVNSSGHGHCQLPPGIPKSSCYIDVRWFPFDVQHCKLFGSWSYGSW 180
 Qy 181 QMQEADISGYIPNGENDLVGIPGKRSERFYECCKEYPDVTFTVMRRRLYYGLNLLIP 240
 Db 181 QMQEADISGYIPNGENDLVGIPGKRSERFYECCKEYPDVTFTVMRRRLYYGLNLLIP 240
 Qy 241 CVLISALALLVFLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLTIAQYFAST 300
 Db 241 CVLISALALLVFLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLTIAQYFAST 300
 Qy 301 MIIVGLSVVTVTVLQYHHHDPDGGKMPKWKTRVILLNWCWFLRMKPGEDKVRPAQCHK 360
 Db 301 MIIVGLSVVTVTVLQYHHHDPDGGKMPKWKTRVILLNWCWFLRMKPGEDKVRPAQCHK 360
 Qy 361 QRRCSLASVEMSAVAPPASNGMLLYIGFRLGLGVHCVPTPDGSGVVCGRMACSPTHDEHL 420
 Db 361 QRRCSLASVEMSAVAPPASNGMLLYIGFRLGLGVHCVPTPDGSGVVCGRMACSPTHDEHL 420
 Qy 421 LHGGQPPGPDPLAKILEEVRYIANFRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
 Db 421 LHGGQPPGPDPLAKILEEVRYIANFRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
 Qy 481 ICTIGILMSAPNFVEAVSKDFA 502
 Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 2

ACH7 MOUSE STANDARD; PRT; 502 AA.

AC P49582;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
 GN CHRNA7 OR ACH7.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALE/c; TISSUE=Brain;
 FX MEDLINE=95324936; PubMed=7601470;
 RA Orr-Urtreger A., Seidlin M.F., Baldini A., Beaudet A.L.;
 RT "Cloning and mapping of the mouse alpha 7-neuronal nicotinic
 acetylcholine receptor.";
 RL Genomics 26:399-402(1995).
 CC -!- FUNCTION: After binding acetylcholine, the ACHR responds by an
 CC extensive change in conformation that affects all subunits and
 CC leads to opening of an ion-conducting channel across the plasma
 CC membrane.
 CC -!- SUBUNIT: Forms a homo-oligomeric channel blocked by alpha-
 CC bungarotoxin. The structure is probably pentameric (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the ligand-gated ionic channel family.
 CC
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 CC
 CC EMBL; L37663; AAC42053.1; -;
 DR PIR; A57175; A57175.
 DR MGI; MGI:99779; Chrna7.
 DR InterPro; IPR006029; Neu channel memb.
 DR InterPro; IPR006202; Neu_chan_IIB.
 DR InterPro; IPR006201; Neu channel.
 DR Pfam; PF02931; Neur chan_IIB; 1.
 DR Pfam; PF02932; Neur chan memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMs; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 KW Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 KW Transmembrane; Multigene family.
 FT SIGNAL 1 22
 FT CHAIN 23 502
 FT BY SIMILARITY.
 FT NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
 FT ALPHA-7 CHAIN. (POTENTIAL).
 FT EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 23 230
 FT TRANSMEM 231 255
 FT TRANSMEM 262 280
 FT TRANSMEM 296 317
 FT POTENTIAL.
 FT DOMAIN 318 469
 FT TRANSMEM 470 490
 FT CYTOPLASMIC (POTENTIAL).
 FT POTENTIAL.
 FT DISULFID 150 164
 FT DISULFID 212 213
 FT BY SIMILARITY.
 FT ASSOCIATED WITH RECEPTOR ACTIVATION
 FT (BY SIMILARITY).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 90 90
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 133 133
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 502 AA; 56631 MW; C9312E5226D120E3 CRC64;
 Query Match 94.3%; Score 2549; DB 1; Length 502;
 Best Local Similarity 94.0%; Pred. No. 2.9e-200;
 Matches 467; Conservative 18; Mismatches 12; Indels 0; Gaps 0;
 QY 6 GGWLAALASLHVSLSQGEFORLYKELVKNYNPLRPVANDSQPLTYVFSLSLIQIMDV 65

Db 6 GGWLAALASLHVSLSQGEFORLYKELVKNYNPLRPVANDSQPLTYVFSLSLIQIMDV 65
 QY 66 DEKNQVLTNTINWLSQMTDHYLVQNVSEYPCVKTRPPDGOIKWPKDILLNNSADDERPDAT 125
 Db 66 DEKNQVLTNTINWLSQMTDHYLVQNVSEYPCVKTRPPDGOIKWPKDILLNNSADDERPDAT 125
 QY 126 FHTNVLNNSGHCQYLPPGIPKSSCYIDVRWFFPDQVCKLKFSGWSYGGMSLDIQMGEA 185
 Db 126 FHTNVLNNSGHCQYLPPGIPKSSCYIDVRWFFPDQVCKLKFSGWSYGGMSLDIQMGEA 185
 QY 186 DISYIINGEWDLVGIPKSRSEYPCVKTRPPDGOIKWPKDILLNNSADDERPDAT 245
 Db 186 DISYIINGEWDLVGIPKSRSEYPCVKTRPPDGOIKWPKDILLNNSADDERPDAT 245
 QY 246 ALALLVLLPADSGEKISLGITVLLSLTVFLLVAEIMPATSDSVPLIAQFAFSTMIIVG 305
 Db 246 ALALLVLLPADSGEKISLGITVLLSLTVFLLVAEIMPATSDSVPLIAQFAFSTMIIVG 305
 QY 306 LSVVTVTVIQLYHHDPDGGKMPKWTIRVILLNWCANFLRMKRPGEKVRPAQCHKPRCS 365
 Db 306 LSVVTVTVIQLYHHDPDGGKMPKWTIRVILLNWCANFLRMKRPGEKVRPAQCHKPRCS 365
 QY 366 LASVEMSAVAPPASNGNLLYIGERGLDGVHCVTDPDGGVVCGRMACSPTHDEHLHGGQ 425
 Db 366 LASVEMSAVAPPASNGNLLYIGERGLDGVHCVTDPDGGVVCGRMACSPTHDEHLHGGQ 425
 QY 426 PPEGDPDLAKLLEEVRYIANFRQDESEAVCSWKFAACVVDRLCLMAFVFTICTIG 485
 Db 426 PEGDPLAKLLEEVRYIANFRQDESEAVCSWKFAACVVDRLCLMAFVFTICTIG 485
 QY 486 ILMGAPNFVEAVSKDFA 502
 Db 486 ILMGAPNFVEAVSKDFA 502

RESULT 3
 ACH7 BOVIN
 ID ACH7 BOVIN STANDARD; PRT; 499 AA.
 AC P54131;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
 GN CHRNA7.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
 RC TISSUE=Adrenal medulla;
 RX MEDLINE=95346009; PubMed=7620615;
 RA Garcia-Guzman M.; Sala F., Sala S., Campos-Caro A., Stuehmer W.,
 Gutierrez L., Criado M.;
 RT "Alpha-Bungarotoxin-sensitive nicotinic receptors on bovine
 chromaffin cells: molecular cloning, functional expression and
 alternative splicing of the alpha 7 subunit.";
 RL Eur. J. Neurosci. 7:647-655(1995).
 CC -!- FUNCTION: After binding acetylcholine, the ACHR responds by an
 CC extensive change in conformation that affects all subunits and
 CC leads to opening of an ion-conducting channel across the plasma
 CC membrane.
 CC -!- SUBUNIT: Forms a homo-oligomeric channel blocked by alpha-
 CC bungarotoxin. The structure is probably pentameric (By
 CC similarity). Homo-oligomer of the short form gives rise to
 CC unfunctional channels, as does coexpression of both long and short
 CC forms of the receptor.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Long;

```
CC      IsoId=P54131-1; Sequence=Displayed;
CC      Name=Short;
CC      IsoId=P54131-2; Sequence=VSP_000075;
CC      TISSUE SPECIFICITY: At least in chromaffin cells.
CC      -!- SIMILARITY: Belongs to the ligand-gated ionic channel family.
CC      -----
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CC      -----
CC      EMBL; X91604; CAA63802.1; -
CC      InterPro; IPR006029; Neu_chan_memb.
CC      InterPro; IPR006202; Neu_chan_LBD.
CC      InterPro; IPR006201; Neu_chan.
CC      Pfam; PF02931; Neu_chan_LBD; 1.
CC      Pfam; PF02932; Neu_chan_memb; 1.
CC      PRINTS; PR00252; NR1ONCHANNEL.
CC      TIGRfams; TIGR00860; LIC; 1.
CC      PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
CC      Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
CC      Transmembrane; Multigene family; Alternative splicing.
CC      KW      1 19
CC      FT      1 19
CC      FT      20 499
CC      FT      CHAIN
CC      FT      20 227
CC      FT      DOMAIN
CC      FT      228 252
CC      FT      TRANSMEM
CC      FT      259 277
CC      FT      TRANSMEM
CC      FT      293 314
CC      FT      TRANSMEM
CC      FT      315 466
CC      FT      DOMAIN
CC      FT      467 487
CC      FT      TRANSMEM
CC      FT      487 487
CC      FT      DISULFID
CC      FT      147 161
CC      FT      209 210
CC      FT      ASSOCIATED WITH RECEPTOR ACTIVATION
CC      FT      (BY SIMILARITY).
CC      FT      N-LINKED (GLCNAC. . .) (POTENTIAL).
CC      FT      N-LINKED (GLCNAC. . .) (POTENTIAL).
CC      FT      N-LINKED (GLCNAC. . .) (POTENTIAL).
CC      FT      N-LINKED (GLCNAC. . .) (POTENTIAL).
CC      FT      VARSPLIC
CC      FT      262 290
CC      FT      Missing (in isoform Short).
CC      FT      /FTid=VSP_000075.
CC      FT      SEQUENCE 499 AA; 56002 MW; AEE5D0B382D042D5 CRC64;
CC      Query Match 94.0%; Score 2540; DB 1; Length 499;
CC      Best Local Similarity 94.6%; Pred. No. 1.6e-199;
CC      Matches 470; Conservative 15; Mismatches 12; Indels 0; Gaps 0;
CC      -----
CC      6 GGVNLAALAAALLHVSLOGEFQKLYKELVKNYNPLERPVANDSPLTVYFSLSLQIMDV 65
CC      3 GSLCLALAASTLHVSLOGEFQKLYKOLVKNYNPLERPVANDSPLTVYFSLSLQIMDV 62
CC      -----
CC      66 DEKNQVLTNTLWQMSWDHVLQNVSEYGVKTVRPDGOIWKPDILLNSADERFAT 125
CC      63 DEKNQVLTNTLWQMTDHLQNVASBPYGVKTVRPDGOIWKPDILLNSADERFAT 122
CC      -----
CC      126 FHTNVLNNSGHCQVLPFGIFKSSCYIDVRFPFDVQCKLKFGSWSYGGSLDLQMQEA 185
CC      123 FHTNVLNNSGHCQVLPFGIFKSSCYIDVRFPFDVQCKLKFGSWSYGGSLDLQMQEA 182
CC      -----
CC      186 DISGVIPIGNDVNLVGIPIKRSERFVECKEYPDVTFTVMRRRTLYGLMLLIPCVLIS 245
CC      183 DISGVIPIGNDVNLVGLKRSERFVECKEYPDVTFTVMRRRTLYGLMLLIPCVLIS 242
CC      -----
CC      246 ALALVFLLPDSGSKISLIGITVLLSLTFVMLLVAEIMPATSDSVPFLAQVPAFTMIIVG 305
CC      243 ALALVFLLPDSGSKISLIGITVLLSLTFVMLLVAEIMPATSDSVPFLAQVPAFTMIIVG 302
CC      -----
CC      306 LSVVVTIVLVQYHHHDPOGKMPKTRVILLNWCWAFLEMRKPGEDKVRPACQHKRRCS 365
CC      303 LSVVVTIVLVQYHHHDPOGKMPKTRVILLNWCWAFLEMRKPGEDKVRPACQHKRRCS 362
CC      -----
CC      366 LASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVCGRMACSPTHDEHLLHGGQ 425
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Db      363 LASVEMSAVAPPATNGNLLYIGFRGLDGMHCAPTDPDSGVCGRVACSTHDEHLLHAGQ 422
Cc      426 PREGPDDILAKILIEVRYTANRPERCODESAVCSSEKFAACVVDRLCLMAFSVFTICTIG 485
Cc      423 PREGPDDILAKILIEVRYTANRPERCODESAVCSSEKFAACVVDRLCLMAFSVFTICTIG 482
Cc      486 ILMSAPNFVEAVSKDFA 502
Cc      483 ILMSAPNFVEAVSKDFA 499
Cc      -----
Cc      RESULT 4
Cc      ACH7 RAT
Cc      ID ACH7 RAT STANDARD; PRT; 502 AA.
Cc      AC Q05941;
Cc      DT 01-FEB-1994 (Rel. 28, Created)
Cc      DT 01-FEB-1994 (Rel. 28, Last sequence update)
Cc      DT 28-FEB-2003 (Rel. 41, Last annotation update)
Cc      DE Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
Cc      GN CHRNA7 OR ACRA7.
Cc      OS Rattus norvegicus (Rat).
Cc      OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Cc      OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
Cc      OX NCBI_TaxID=10116;
Cc      RN [1]
Cc      RP SEQUENCE FROM N.A.
Cc      RC TISSUE=Brain;
Cc      RX MEDLINE=93147931; PubMed=7678857;
Cc      RA Seguela P., Wadiche J., Dineley-Miller K., Dani J.A., Patrick J.W.;
Cc      RT "Molecular cloning, functional properties, and distribution of rat
Cc      RT brain alpha 7: a nicotinic cation channel highly permeable to
Cc      RT calcium.";
Cc      RL J. Neurosci. 13:596-604(1993).
Cc      RN [2]
Cc      RP SEQUENCE FROM N.A.
Cc      RC STRAIN=Sprague-Dawley; TISSUE=Brain;
Cc      RA Boulter J.;
Cc      RN Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
Cc      [3]
Cc      RP REVISION TO 363.
Cc      RC STRAIN=Sprague-Dawley; TISSUE=Brain;
Cc      RA Hartley M.;
Cc      RN Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
Cc      CC -!- FUNCTION: After binding acetylcholine, the AChR responds by an
Cc      CC extensive change in conformation that affects all subunits and
Cc      CC leads to opening of an ion-conducting channel across the plasma
Cc      CC membrane.
Cc      CC -!- SUBUNIT: Forms a homo-oligomeric channel blocked by alpha-
Cc      CC bungarotoxin. The structure is probably pentameric (By
Cc      CC similarity).
Cc      CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
Cc      CC -!- SIMILARITY: Belongs to the ligand-gated ionic channel family.
Cc      -----
Cc      This SWISS-PROT entry is copyright. It is produced through a collaboration
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Cc      entities requires a license agreement (see http://www.isb-sib.ch/announce/
Cc      or send an email to license@isb-sib.ch).
Cc      -----
Cc      EMBL; S53987; AAB25224.2; -
Cc      EMBL; L31619; AAC33136.1; -
Cc      PIR; T01378; T01378.
Cc      InterPro; IPR006029; Neu_chan_memb.
Cc      InterPro; IPR006202; Neu_chan_LBD.
Cc      InterPro; IPR006201; Neu_chan.
Cc      Pfam; PF02931; Neu_chan_LBD; 1.
Cc      Pfam; PF02932; Neu_chan_memb; 1.
Cc      PRINTS; PR00252; NR1ONCHANNEL.
Cc      TIGRfams; TIGR00860; LIC; 1.
Cc      PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
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KW Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW Transmembrane; Multigene family.
FT SIGNAL 1 22
FT CHAIN 23 502
FT
FT DOMAIN 23 230
FT TRANSMEM 231 255
FT TRANSMEM 262 280
FT TRANSMEM 296 317
FT DOMAIN 318 469
FT TRANSMEM 470 490
FT DISULFID 150 164
FT DISULFID 212 213
FT CARBOHYD 46 46
FT CARBOHYD 90 90
FT CARBOHYD 133 133
FT CONFLICT 447 447
FT CONFLICT 469 469
SQ SEQUENCE 502 AA; 56410 MW; 00996E74EC7B9A56 CRC64;
Query Match 93.8%; Score 2535; DB 1; Length 502;
Best Local Similarity 93.6%; Pred. No. 4e-199;
Matches 465; Conservative 18; Mismatches 14; Indels 0; Gaps 0;
QY 6 GGVWLAALASLHVSLQSGFQRLKYLKYNPLRPVANDSQPLTVVFSLSLLQIMDV 65
Db 6 GGVWLAALASLHVSLQSGFQRLKYLKYNPLRPVANDSQPLTVVFSLSLLQIMDV 65
QY 66 DEKNQVLTNIWLQSWTDHYLQNNVSEYGVKTVRFDGQIWKPDILLYNSADRFDAT 125
Db 66 DEKNQVLTNIWLQSWTDHYLQNNVSEYGVKTVRFDGQIWKPDILLYNSADRFDAT 125
QY 126 FHTNVLNNSGHCQVLPPIKSSCIDVRWPFVDVQCKLFGSWSGVGSLDLQMOEA 185
Db 126 FHTNVLNNSGHCQVLPPIKSSCIDVRWPFVDVQCKLFGSWSGVGSLDLQMOEA 185
QY 186 DISGYIPNGEWDVIGPKRSRFEYCKEPPDVTFTVMRRRTLYXGLNLLIPCVLIS 245
Db 186 DISGYIPNGEWDVIGPKRSRFEYCKEPPDVTFTVMRRRTLYXGLNLLIPCVLIS 245
QY 246 ALAILVFLPADSGKISLIGITVLSLTVFMLLVAEIMPATSDSVPLIAQYFASTMIIVG 305
Db 246 ALAILVFLPADSGKISLIGITVLSLTVFMLLVAEIMPATSDSVPLIAQYFASTMIIVG 305
QY 306 LSVVTVIVLVYHHDDPDGCKMPKTRVILLNWCANFLMKPBGDKVPAQCHKQRCS 365
Db 306 LSVVTVIVLVYHHDDPDGCKMPKTRVILLNWCANFLMKPBGDKVPAQCHKQRCS 365
QY 366 LASVEMSAVAPPASNGNLLYTGFRGLDGVHCVPTPDGSGVCGRMACSPTHDEHLLHGQ 425
Db 366 LASVEMSAVAPPASNGNLLYTGFRGLDGVHCVPTPDGSGVCGRMACSPTHDEHLLHGQ 425
QY 426 PPEGDPDLAKILEEVRVYIANTFRCDSEAVCEMKFACVVDRLCLMAFSVFTIICITG 485
Db 426 PPEGDPDLAKILEEVRVYIANTFRCDSEAVCEMKFACVVDRLCLMAFSVFTIICITG 485
QY 486 ILMSPNFVEAVSKDFA 502
Db 486 ILMSPNFVEAVSKDFA 502

RESULT 5

ID ACH7_CHICK
AC P2270;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=91097796; PubMed=1702646;
RA Couturier S., Bertrand D., Matter J.M., Hernandez M.C., Bertrand S., Millar N., Valera S., Barkas T., Ballivet M.;
RT "A neuronal nicotinic acetylcholine receptor subunit (alpha 7) is developmentally regulated and forms a homo-oligomeric channel blocked by alpha-BTX.";
RL Neuron 5:847-856(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=90315158; PubMed=2369519;
RA Schoeffer R., Conroy W.G., Whiting P., Gore M., Lindstrom J.;
RT "Brain alpha-bungarotoxin binding protein cDNAs and MBs reveal subtypes of this branch of the ligand-gated ion channel gene superfamily.";
RL Neuron 5:35-48(1990).
RN [3]
RP SEQUENCE OF 1-18 FROM N.A.
RC STRAIN=White leghorn; TISSUE=Erythrocyte;
RX MEDLINE=93049204; PubMed=1425587;
RA Matter J.M.;
RT "Neuronal specificity of the alpha 7 nicotinic acetylcholine receptor promoter develops during morphogenesis of the central nervous system.";
RL EMBO J. 11:4529-4538(1992).
RN [4]
RP SEQUENCE OF 24-47.
RC TISSUE=Brain;
RX MEDLINE=85270494; PubMed=3860855;
RA Conti-Troconi B.M., Dunn S.M.J., Barnard E.A., Dolly J.O., Lai F.A., Ray N., Raftery M.A.;
RT "Brain and muscle nicotinic acetylcholine receptors are different but homologous proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:5208-5212(1985).
RN [5]
RP MUTAGENESIS OF LSU-270.
RX MEDLINE=92047932; PubMed=1719423;
RA Recah P., Bertrand D., Galzi J.-L., Devillers-Thiery A., Mulle C., Hussey N., Bertrand S., Ballivet M., Changeux J.-P.;
RT "Mutations in the channel domain alter desensitization of a neuronal nicotinic receptor.";
RL Nature 353:846-849(1991).
RN [6]
RP MUTAGENESIS TO CONVERT ION SELECTIVITY FROM CATIONIC TO ANIONIC.
RX MEDLINE=93024917; PubMed=1383829;
RA Galzi J.-L., Devillers-Thiery A., Hussey N., Bertrand S., Changeux J.-P., Bertrand D.;
RT "Mutations in the channel domain of a neuronal nicotinic receptor convert ion selectivity from cationic to anionic.";
RL Nature 359:500-505(1992).
CC -!- FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma membrane.
CC -!- SUBUNIT: Forms a homo-oligomeric channel blocked by alpha-bungarotoxin. The structure is probably pentameric (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- DEVELOPMENTAL STAGE: Alpha-7 transcripts transiently accumulate in the developing optic tectum between E5 and E16.
CC -!- SIMILARITY: Belongs to the ligand-gated ionic channel family.
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Db      487 PTLVD 491

RESULT 8
ACH2 HUMAN
ID ACH2_HUMAN STANDARD; PRT; 529 AA.
AC Q15822; O9HAQ3;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuronal acetylcholine receptor protein, alpha-2 chain precursor.
GN CHRNA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hypothalamus;
RX MEDLINE=97062879; PubMed=8906617;
RA Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,
RA Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.;
RT "Comparative structure of human neuronal alpha 2-alpha 7 and beta
RT 2-beta 4 nicotinic acetylcholine receptor subunits and functional
RT expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
RT beta 4 subunits."
RL J. Mol. Neurosci. 7:217-228(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC Groot Kormelink P.J.;
RA Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Blechschmidt K., Rosenthal A.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: After binding acetylcholine, the AChR responds by an
CC extensive change in conformation that affects all subunits and
CC leads to opening of an ion-conducting channel across the plasma
CC membrane.
CC -!- SUBUNIT: Neuronal AChR seems to be composed of two different types
CC of subunits: alpha and non-alpha (beta). Alpha-2 subunit can be
CC combined to beta-2 or beta-4 to give rise to functional receptors.
CC -!- SURCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the ligand-gated ionic channel family.
CC
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; U62431; ABA40109.1; -.
CC EMBL; Y16281; CAA76154.1; -.
CC EMBL; AF311103; -, NOT ANNOTATED_CDS.
CC Genew; HGNC:1956; CHRNA2.
CC MIM; 118502; -.
CC DR GO; GO:0005892; C:nicotinic acetylcholine-gated receptor-chan. . .; TAS.
CC DR GO; GO:0015464; F:acetylcholine receptor activity; TAS.
CC DR GO; GO:0004889; F:nicotinic acetylcholine-activated cation-se. . .; TAS.
CC DR GO; GO:0007165; F:signal transduction; TAS.
CC DR GO; GO:0007268; F:synaptic transmission; TAS.
CC DR InterPro; IPR006029; Neur_chan_IIBD.
CC DR InterPro; IPR006201; Neur_chan_IIBD.
CC DR Pfam; PF02931; Neur_chan_IIBD; 1.
CC DR Pfam; PF02932; Neur_chan_IIBD; 1.
CC DR PRINTS; PR00252; NRIONCHANNEL.
CC DR TIGRFAMs; TIGR00860; LIC; 1.
CC DR PROSITE; PS00236; NEUROTRF_ION_CHANNEL; 1.
CC DR Postsynaptic membrane; Ionic Channel; Glycoprotein; Signal;
KW

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```

KW Transmembrane; Multigene family.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 529 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
FT ALPHA-2 CHAIN.
FT DOMAIN 27 264 EXTRACELLULAR.
FT TRANSMEM 265 289 POTENTIAL.
FT TRANSMEM 297 315 POTENTIAL.
FT TRANSMEM 331 352 POTENTIAL.
FT DOMAIN 353 502 CYTOPLASMIC.
FT TRANSMEM 503 521 POTENTIAL.
FT DISULFID 183 197 BY SIMILARITY.
FT DISULFID 247 248 ASSOCIATED WITH RECEPTOR ACTIVATION
FT CARBOHYD 79 79 (BY SIMILARITY).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 125 125 A > T (IN REF. 3). (POTENTIAL).
SQ SEQUENCE 529 AA; 59735 MW; 7F512B06CCD9A9FD CRC64;

Query Match 35.1%; Score 949; DB 1; Length 529;
Best Local Similarity 40.0%; Pred. No. 9.3e-70;
Matches 201; Conservative 78; Mismatches 159; Indels 64; Gaps 9;

Qy 24 EFORKLYKELVKNYNPLERPVANDSQPLTVYFSLSLLOINDVDEKQVLTNTLWLSWT 83
Db 57 ETEDELFLKHLFRGYNRWAREVPNTSDVIVRFGLSIAQLIDVDKQNMVTTNWLKQWS 116
Qy 84 DHVLOQNVSEYPGVKTVRFPDGOIKWPKDILLYNADRRPDATFTNTLVNNSGHCYLP 143
Db 117 DYKLRNPADFGNITSRLVSEMIWIPDIVLYNADGEFAVTMTKAHLSTGTVHWVPP 176
Qy 144 GIFKSCYIDVRWFPDVOHCKLFGSGWSYGGSLDLQMOE--ADISGYIPNGEWDLVGI 201
Db 177 AIYKSSCSIDVTFPPDQCKMKFGSWTYDKAKIDLEQMEQTVDLKDYWESGEWLVNA 236
Qy 202 PKRSERFYECCKEYPDVTFVTMRRRTLYGNNLLIPCVLSALALLVLLPADSGEK 261
Db 237 TGTYSKKYDCCABIYDPVTYAFVIRLPLFTINLIIPCLLSCLTVLVYFLPSDCGEK 296
Qy 262 ISLIGITVLLSLTVFMILLVAIMPATSDSVPLIAQYFASMTIIVGLSVVTVIVLYQHH 321
Db 297 ITICISVLLSLTVFLLITELIISTSLVPLIGEYLLFTMTFTLSIVIVFVNLVHRS 356
Qy 322 PDGKMPKTRVILLNWCAMFLRMKRPGEKDVPAQOHKQRCORCSLASVMSAVPPASN 381
Db 357 PSTHTMHWVRGALLGCVPRWLLNRP-----PPVEL 389
Qy 382 GNLLYI-----GFRGLDG-----VHCVPDPDSGVVGRMA-----CSPTHDEHLHGG 424
Db 390 CHPLRLKLSYHWNLESNVDAEREVVVEEDRWACAGHVAPSVGTLCSHG-----LHSG 445
Qy 425 QP-----PEGD-----PDLAKILEVRYIANRFRQDESEAVCSWKFAACVYDLRL 472
Db 446 ASGPKAEALLQEGELLSPHMQALEGVHVIADHLRSEDADSSVKEDKWYVMVIDRIFL 505
Qy 473 MAFSVFTIITIGILMSAPNFV 494
Db 506 WLFTIVCFGLGTIGLFL--PPFL 525

RESULT 9
ID ACH1_SCHGR STANDARD; PRT; 557 AA.
AC P23414;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acetylcholine receptor protein, alpha-1 chain precursor.
OS Schistocerca gregaria (Desert locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Cyrtacanthacridinae; Schistocerca.
OX NCBI_TaxID=7010;

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EMBL; M20293; AAA40664.1; JOINED.
EMBL; M20294; AAA40664.1; JOINED.
EMBL; M20295; AAA40664.1; JOINED.
EMBL; M20296; AAA40664.1; JOINED.
PIR; A40110; A40110.
DR InterPro; IPR006029; Neu_chan_memb.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006201; Neur_chan_LBD.
PFam; PF02931; Neur_chan_LBD; 1.
DR PFam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NR1ONCHANNEL.
DR TIGRFAWS; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW Transmembrane; Multigene family.
FT SIGNAL 1 27
FT CHAIN 28 511
FT
FT DOMAIN 28 241
FT TRANSMEM 242 266
FT TRANSMEM 274 292
FT TRANSMEM 308 329
FT DOMAIN 330 484
FT CYTOPLASMIC 485 503
FT TRANSMEM 485 503
FT DOMAIN 391 402
FT DISULFID 160 174
FT
FT CARBOHYD 56 56
FT CARBOHYD 106 106
FT CARBOHYD 212 212
FT CONFLICT 494 494
FT CONFLICT 511 AA; 58611 MW; 382483B901D613B CRC64;
SQ SEQUENCE 511 AA; 58611 MW; 382483B901D613B CRC64;
Query Match 35.0%; Score 944.5; DB 1; Length 511;
Best Local Similarity 39.1%; Pred. No. 2.1e-69;
Matches 202; Conservative 82; Mismatches 179; Indels 53; Gaps 9;
Qy 8 VW--LALAASLLHVSQGEFORKLYKELAKVKNYFLERPVANDSOPLTVYFSLSLQIMDV 65
Db 16 LWCLLVFAVLTVQQGSHTHAEDRLFKHFGGYNWARVPVNTSDVIVRFGLSIAQLIDV 75
Qy 66 DEKQVLTNNLQMSWDHYLQNVSEYPGKIVRPPDGOIWKPDILLNSADERDAT 125
Db 76 DEKQVMTNNLQMSWDHYLQNVSEYPGKIVRPPDGOIWKPDILLNSADERDAT 135
Qy 126 FHTNVLNNSGHCVOYLPFGIEKSCYIDVRFPDQVCKLFGSWSYGSWLDLQOE- 184
Db 136 HMTKAHLFFTGTVHVPVPAIYKSSCIDVTFPPDQCKKFGSWTYDXAKIDLEQWER 195
Qy 185 -ADISGYIPNGEWDLVGIPGKRSEFYECCKEYPPDVFTVTMRRTLYYGLNLLIPCVL 243
Db 196 TVDLKDYWESGEWALINATGYNKKYDCCAEIYPDVTVYFVIRRLPLFTYINLIIPCLL 255
Qy 244 ISALALVFLPADSGEKISLGLTVLLSLVFMILVAIMPATSVDSEVLIQYFASMTII 303
Db 256 ISCLTVLVFLYLPSECGEKITCLISVLLSLVFMILVAIMPATSVDSEVLIQYFASMTII 315
Qy 304 VGLSVVTVVIVLQVHHDPDGGKMPKTRVILLNWCAMFLRMKRP-----GEDKVRPA 356
Db 316 VTLISVITVVLNVHRSFSTHNMENWVRVALLGVRPRLMMNRPLPFWMLHGSFDLXLS 375
Qy 357 COHKORRCSLASVEMSAVAPPASNGNLLYTGFRGLDGVCHVCPPTDS--GVVCGRMACSP 414
Db 376 PSYHMLETMDAGEREEETEEEDENICV-----CAGLPDSSMGVLYG----- 420
Qy 415 THDEHLLGG-----QPEG-----DPLAKILEVRYIANFRQDSSEAVCS 458
Db 421 -----HGLHLRAMEPETKTPSOASBILISPOIQKALEGVHYIADLRSEDADSVKE 473
Qy 459 EWKFAACVVDRLCLMAFVFTTICTIGTIGLMSAPNEV 494
Db 474 DKYVAMVVDRLCLMAFVFTTICTIGTIGLMSAPNEV 507

RESULT 11
ACCH CARAU
ID ACCH CARAU STANDARD; PRT; 459 AA.
AC P19370;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuronal acetylcholine receptor protein, beta-2 chain (GF-beta-2) (Fragment).
DE Carassius auratus (Goldfish).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=90384858; PubMed=2402468;
RA Hieber V.C., Bouchev J.E., Agranoff B.W., Goldman D.;
RT "Nucleotide and deduced amino acid sequence of the goldfish neural
nicotinic acetylcholine receptor beta-2 subunit.";
RL Nucleic Acids Res. 18:5307-5307(1990)
CC -|- FUNCTION: After binding acetylcholine, the AChR responds by an
extensive change in conformation that affects all subunits and
leads to opening of an ion-conducting channel across the plasma
membrane.
CC -|- SUBUNIT: Neuronal AChR seems to be composed of two different type
of subunits: alpha and non-alpha (beta).
CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
CC -|- SIMILARITY: Belongs to the ligand-gated ionic channel family.
CC
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CC
EMBL; X54052; CAA37986.1; -
PIR; S14703; S14703. Neu_chan_memb.
DR InterPro; IPR006029; Neur_chan_LBD.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006201; Neur_chan_memb; 1.
PFam; PF02931; Neur_chan_LBD; 1.
PFam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NR1ONCHANNEL.
DR TIGRFAWS; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein;
KW Transmembrane; Multigene family.
FT NON_TER 1 203
FT DOMAIN <1 203 EXTRACELLULAR.
FT TRANSMEM 204 228
FT TRANSMEM 236 254
FT TRANSMEM 270 291
FT DOMAIN 292 421
FT TRANSMEM 422 440
FT CARBOHYD 21 21
FT DISULFID 125 139
FT CARBOHYD 138 138
SQ SEQUENCE 459 AA; 53040 MW; 860B1A011AA47CF6 CRC64;
Query Match 34.9%; Score 942.5; DB 1; Length 459;
Best Local Similarity 38.7%; Pred. No. 2.6e-69;
Matches 190; Conservative 95; Mismatches 141; Indels 65; Gaps 8;
Qy 35 KYNPLRPVANDSQPLTVYFSLSLQIMDVDEKQVLTNNLQMSWDHYLQNVSEY 94
Db 10 ERYNKLIRPAVNVKQQVTIGIKVSLAQISNREQIMTNVWLTQETDYLVDPEY 69

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QY 95 PGKTVRPDGOIWKPDILLVNSADDERPDATHTHTVNLVNSGHCQVLPFGPKSCYIDV 154
Db 70 EGKILRPSQSIHWLDPEDIVLNNADGVVEVSFCYNAVVSNTGDIIFWLPFPAIYKSAIEV 129
QY 155 RWFPPDVQCKLKPGSWSYGGSLDLOMGE--ADISGXIYPNGEWDLVGIPGKRSERFYEC 212
Db 130 RNFPPDQNCITKFSWYDRTELDDVLTSDFASRDDYTPSGEWDIVSLPGRKNE----- 184
QY 213 CKEP-----YPDVFTVTRRRRTLYXGLNLLIPCVLISALALVFLPADSGEKISLIGITV 268
Db 185 --DPNDLATYDITDYFVKRKEFLFTINLIIPCVLITSLAILVFLYPSDCGKVKVLSV 242
QY 269 LLSLVEMLLVVAIMEAPSDSVPLIAQYFASPMIIVGLSVVTVIVLVQVHHDDPGKMP 328
Db 243 LLALVFLLSIKSIVPPTSLAVPLIGKYLMTWLVTSIVTSVCLVNVHRSPTTHMP 302
QY 329 KWTIRVILLNCAWFLMRKRPDGVKVPACQHKQRRCSLASVMSAVAPPASNGNLLYIG 388
Db 303 EMVKCVFLHKLPAFLLMRPGSRNVRPRRKHQRKSFSSHQ----- 344
QY 389 FRGLDGVHCVPPTDPSGVVCGRMACSPTHDEHLLHGGQPPEG-----DPDLAKIL 437
Db 345 ----DGDSFFLTDGPRVCGAWRV-----GDLPEGSEFRQVRKVRHDQVDDEAI 389
QY 438 EEVRYIANFRQDSEASEVCSWKFAACVVDLCLMAFSVFTIICITIGILMSAPNP----- 493
Db 330 DGVRIAEHMKIEDDEGLIEDKVKYVAMVIDRLFLWIFLVCVGVTLGLFVQ-PLFQSYN 448
QY 494 ---VEAVSKDF 501
Db 449 TPVAEEVYGF 459

RESULT 12
ACH2 CHICK
ID ACH2 CHICK STANDARD; PRT; 528 AA.
AC P09480;
AT TISSUE=Brain;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuronal acetylcholine receptor protein, alpha-2 chain precursor.
OS Gallus gallus (Chicken).
OC Archosauria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=88283624; PubMed=3267226;
RA Nef P., Oneyser C., Alliod C., Couturier S., Ballivet M.;
RT "Genes expressed in the brain define three distinct neuronal
RL nicotinic acetylcholine receptors."
CC EMO J. 7:595-601(1988).
CC -!- FUNCTION: After binding acetylcholine, the AChR responds by an
CC extensive change in conformation that affects all subunits and
CC leads to opening of an ion-conducting channel across the plasma
CC membrane.
CC -!- SUBUNIT: Neuronal AChR seems to be composed of two different
CC type of subunits: alpha and non-alpha (also called beta). A
CC functional receptor seems to consist of two alpha-chains and
CC three non-alpha chains
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the ligand-gated ionic channel family.
CC
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DR EMBL; X07339; CAB59645.1; -
DR EMBL; X07340; CAB59645.1; JOINED.
DR EMBL; X07341; CAB59645.1; JOINED.
DR EMBL; X07342; CAB59645.1; JOINED.
DR EMBL; X07343; CAB59645.1; JOINED.
DR EMBL; X07344; CAB59645.1; JOINED.
DR EMBL; AJ250360; CAB59625.1; -.
DR PIR; S00377; ACCH2N.
DR InterPro; IPR006029; Neu_chan_memb.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006201; Neur_chan_LBD.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR PRINTS; PR00252; Neur_chan_LBD; 1.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW Transmembrane; Multigene family.
FT SIGNAL 1 23
FT CHAIN 24 528
FT DOMAIN 24 239
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FT TRANSMEM 272 290
FT TRANSMEM 306 327
FT DOMAIN 328 501
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FT DOMAIN 394 410
FT DISULFID 158 172
FT DISULFID 222 223
FT CARBOHYD 54 54
FT CARBOHYD 104 104
SQ SEQUENCE 528 AA; 60675 MW; E76C6360AF876364 CRC64;

Query Match 34.8%; Score 941.5; DB 1; Length 528;
Best Local Similarity 38.0%; Pred. No. 3.8e-69;
Matches 201; Conservative 85; Mismatches 174; Indels 69; Gaps 10;

QY 8 VWLAL--AASLLVSLQGERQKLYKELVKNYPLRPVANDSQPLVYFSLSLQIMD 64
Db 13 VWCFTVLAQATREKQPHGPAEDRLKFLFTGYNRWSRPVNTSDVVLKGLSIAQLID 72
QY 65 VDEKNQVLTNNIQLQMSWTDHYLQWNVSEYPGVKTVRFPDGGIWKPDILLNSADERFDA 124
Db 73 VDEKNQMTTNNVWLKQWSDYKLWNPDPEDFNVTISIRVSEMIWIPDIVLYNNADGEAV 132
QY 125 THTNVLVNSGHCQVLPFGPKSCYIDVWFFPDVHOCHKLFGSWSYGGSLDLOMGE 184
Db 133 THMTRKHLFSGKVKWVFPALYKSSCSIDVTYFFPDQNCCKMKFGSWTYDKAKIDLENME 192
QY 185 --ADISGYIPNGEWDLVGIPGKRSERFYECCKEYPPDVFTVTRRRRTLYVGLNLLIPCV 242
Db 193 HHVDLKQWYSEGEWAIINAIGYNSKKYDCCTEYIPDITFYFVIRRLPLFTINLIIPCL 252
QY 243 LISALALLVFLPADSGEKISLIGITVLSLVFVLMVAEIMPATSDSVPLIAQYFASPMI 302
Db 253 LISCLTVLFLPSDCGKIKTLCISVLLSLTVLFLITETIIPSTSLVPLIGEYLLFTMI 312
QY 303 IVGLSVVTVIVLVQVHHDDPGGKMPKTRVILLNCAWFLMRK-----PGEKV----- 353
Db 313 FVLISIIITVFLNVHRSPTHTMPHWRSFFLGFIPRWLFMRKRPALLPAEGTGTQYD 372
QY 354 RPAQCHKQRCSLAS-----VMSAVAPPASNGNLLYIGRGLDG 394
Db 373 PPGTFLSTRCLWLTDDVDKWEEREEEEEEEEEEKAYPSRVPSC-----GSQG 424
QY 395 VHCVPTPDGSGVYCGRMACSPTHDEHLLHGGQPPE-----GD-----PDLAKILEE 439
Db 425 TQC-----HYSCERQAKAS-----GGPAPQVPLKGEVSGDQGLTSLPSILALEG 471
QY 440 VRYIANFRQDSEASEVCSWKFAACVVDRLCLMAFSVFTIICITIGIIM 488

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OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN
 RP SEQUENCE FROM N.A.
 RC TISSUE=Head;
 RX MEDLINE=90353591; PubMed=2117557;
 RA Jonas P., Baumann A., Merz B., Gundelfinger E.D.;
 RT "Structure and developmental expression of the D alpha 2 gene
 encoding a novel nicotinic acetylcholine receptor protein of
 Drosophila melanogaster";
 RT Drosophila melanogaster";
 RL Nucleic Acids Res. 18:3640-3640(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Head;
 RX MEDLINE=90353591; PubMed=2117557;
 RA Jonas P., Baumann A., Merz B., Gundelfinger E.D.;
 RT "Structure and developmental expression of the D alpha 2 gene
 encoding a novel nicotinic acetylcholine receptor protein of
 Drosophila melanogaster";
 RT Drosophila melanogaster";
 RL Nucleic Acids Res. 18:3640-3640(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Head;
 RX MEDLINE=90360975; PubMed=1697262;
 RA Sawruk E., Schloss P., Betz H., Schmitt B.;
 RT "Heterogeneity of Drosophila nicotinic acetylcholine receptors: SAD,
 a novel developmentally regulated alpha-subunit";
 RL EMBO J. 9:2671-2677(1990).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Fandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
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 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
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 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laoko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Martel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler P., Shen H.,
 RA Shue B.C., Siden-Kianos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley; TISSUE=Head;
 RX MEDLINE=22426066; PubMed=12537569;
 RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
 RA George R.A., Guarin H., Krommiller B., Pacle J.M., Park S., Wan K.H.,
 RA Rubin G.M., Ceiniker S.E.;
 RT "A Drosophila full-length cDNA resource";
 RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
 CC
 CC -!- FUNCTION: After binding acetylcholine, the AChR responds by an
 CC extensive change in conformation that affects all subunits and
 CC leads to opening of an ion-conducting channel across the plasma
 CC membrane.
 CC
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC
 CC -!- TISSUE SPECIFICITY: CNS in embryos.
 CC
 CC -!- DEVELOPMENTAL STAGE: Late embryonic and late pupal stages.
 CC
 CC -!- SIMILARITY: Belongs to the ligand-gated ionic channel family.
 CC
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 CC
 CC
 CC EMBL; X52274; CAA36517.1; -;
 CC EMBL; X53583; CAA37652.1; -;
 CC EMBL; AE003748; AAF56303.1; -;
 CC EMBL; AY058446; AAL13675.1; -;
 CC PIR; S11679; ACFFA2.
 CC Flybase; FBgn0000039; nAChR-alpha-96Ab.
 CC InterPro; IPR006029; Neu_chan_memb.
 CC InterPro; IPR006202; Neur_chan_LBD.
 CC InterPro; IPR006201; Neur_chan_LBD.
 CC Pfam; PF02931; Neur_chan_LBD; 1.
 CC Pfam; PF02932; Neur_chan_memb; 1.
 CC PRINTS; PR00252; NRIONCHANNEL.
 CC TIGRFAMs; TIGR00860; LIC; 1.
 CC PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 CC Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 CC Transmembrane; Multigene family.
 CC SIGNAL 1 21 PROBABLE.
 CC CHAIN 22 576 ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-
 CC LIKE CHAIN 2.
 CC DOMAIN 22 261 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 262 285 POTENTIAL.
 CC TRANSMEM 293 311 POTENTIAL.
 CC TRANSMEM 327 346 POTENTIAL.
 CC DOMAIN 347 526 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 527 545 POTENTIAL.
 CC DISULFID 169 183 BY SIMILARITY.
 CC DISULFID 243 244 ASSOCIATED WITH RECEPTOR ACTIVATION
 CC (BY SIMILARITY).
 CC CARBOHYD 65 65 N-LINKED (GLCNAC. .) (POTENTIAL).
 CC CARBOHYD 254 254 N-LINKED (GLCNAC. .) (POTENTIAL).
 CC CARBOHYD 570 570 N-LINKED (GLCNAC. .) (POTENTIAL).
 CC SEQUENCE 576 AA; 65506 MW; 97D6A46CAD3CF42F CRC64;
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 Query Match 34.7%; Score 937.5; DB 1; Length 576;
 Best Local Similarity 38.1%; Pred No. 8.9e-69;
 Matches 203; Conservative 103; Mismatches 184; Indels 43; Gaps 9;
 QY 3 CSPGVWLAALASLHVSLOGE-FQKLYKELVKNYFLERPVANDSQPLTVYFSLSLQ 61
 Db 23 CKP--LCCLLVLLLCETVQAPDAKRLYDLLSNYNRLIRFVSNNTDVLVGLRLSQ 80
 QY 62 IMDVDEKQVLTNNIWLQMSWTDHYLVQNVSEYGVKTVRFPDGOIWPDIILYNSADER 121
 Db 81 LIDLMLKQDILTTNVWLESHQDKFKWDPSEYGVGVTELYVPSHILWLPDIYLNADGE 140
 QY 122 FDATEFTNVLNSSHCHCOYLPGLFKSCYIDVRFDPVOHCKLKFQSMVSGWSDL- 180
 Db 141 YVVTMTKAILHYTGKVVTPPAIFKSSCEIDVRYFFPDQQTCFMKFGSVTDGQIDLK 200
 QY 181 ---QMGE-----ADISGYPNGEMLVIGPKGRSFRFYECCKEYPDVTFVTMERR 229


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DR EMBL; U62432; AAB40110.1; -.
DR EMBL; Y08418; CAA69695.1; -.
DR EMBL; AJ007783; CAA07682.1; -.
DR EMBL; AJ007784; CAA07682.1; JOINED.
DR EMBL; AJ007785; CAA07682.1; JOINED.
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DR EMBL; AJ007787; CAA07682.1; JOINED.
DR EMBL; BC001642; AAH01642.1; -.
DR EMBL; BC002996; AAH02996.1; -.
DR EMBL; BC000513; AAH00513.1; -.
DR EMBL; AF385584; AAK68110.1; -.
DR EMBL; X53559; CAA37625.1; -.
DR PIR; A37040; A37040.
DR PIR; A53956; A53956.
DR Genew; HGNC:1957; CHRNA3.
DR MIM; 118503; -.
DR GO; GO:0005892; C:nicotinic acetylcholine-gated receptor-chan. . .; TAS.
DR GO; GO:0015464; F:acetylcholine receptor activity; TAS.
DR GO; GO:0004889; F:nicotinic acetylcholine-activated cation-se. . .; TAS.
DR GO; GO:0005215; F:transporter activity; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR GO; GO:0006810; P:transport; TAS.
DR InterPro; IPR006029; Neu channel memb.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006201; Neur_chan_LBD.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUOTR_ION_CHANNEL; 1.
DR Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW Transmembrane; Multigene family; Alternative splicing; Polymorphism.
FT SIGNAL 1 29
FT CHAIN 30 503
FT DOMAIN 30 238
FT TRANSMEM 239 263
FT TRANSMEM 271 289
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FT DOMAIN 327 475
FT TRANSMEM 476 495
FT DISULFID 157 171
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FT CARBOHYD 53
FT CARBOHYD 170 170
FT VARSPIC 1 5
FT VARIANT 21 21
FT CONFLICT 5 13
FT CONFLICT 11 14
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SQ SEQUENCE 503 AA; 57309 MW; 8A9EBC5D71AEC7D6 CRC64;

Query Match 34.6%; Score 936; DB 1; Length 503;
Best Local Similarity 37.7%; Pred No. 1e-68;
Matches 189; Conservative 94; Mismatches 164; Indels 54; Gaps 7;

Qy 10 LALAASLHVSLOGEFORLYKELKYNINPLERPVANDSQELTYVYFSLSLQIMDVDEKN 69
Db LLLALLSLLPVARASEAERHLEFELFEDYNEIRPVANVSDPVIITHFEVMSQLVKVDEVN 76
Qy 70 QVLTINWLQMSWDHYLQWNVSEYPGVKTFRFPDQIWKPDILLYNSADERPDAFTTN 129
Db QIMETNLWLKQIWDYKLNWPSDYGGAEFMRVPAQKIWKPDIVLYNNVAGDFQVDDKTK 136
Qy 130 VLNVSSGHGQYLPGIIFKSSCYIDVRFPFVQHCCKLAFGSGSYGWSLDLQW--QEADI 187
Db ALLXYTGEVTWIPPAIFAKSKIDVTYFPFDYQNCMTKFGWSYDKAKIDLVLIGSSMNL 196

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Qy 188 SGYPNGEWDLVGIPGK3SERFECCKEYPDVTFVTMRRTLYYGLNLLIPCVLISAL 247
Db 197 KDYWESGEWAIKAPGXHDIKYKNCCEIYDIIYSYIRRLPLFYINLLIPCLLSFL 256
Qy 248 ALLVFLPADSGEKISLGIITVLLSLTVFMLVAEIMPATSDSVELIAQYFASFTMIIVGLS 307
Db 257 TVLVFYLPSDCGEKVTLCISVLLSLTVFLLVITETIPSTSLVIPLEIGYLLFTMIFVTL 316
Qy 308 VVTVIVLQYHHHDPDGGKMPKWTVRVILLNWCWFLRMKBPGEKVRPACQHKQRCCLA 367
Db 317 IVITFVLNHYRTPTTHTMPSWKTVFLNLLPRVFMFTRP-----T 358
Qy 368 SVMSAVAPPPASNGNLLYIGFRLDGVHCVPTPDS-----GVVCGRMACSPTHDEHL-- 420
Db 359 SNEGNAQKPRPLYGAE-----LSNLCFSRAESKGCKEGYPCQDGMCGYCHRRIKI 410
Qy 421 -----LHGQPPPEG-----DPLAKILEEVRYIANRFRQDESEAVCSWEKFAA 464
Db 411 SNFSANLTRSSSESVDVLSLSALSPEIKAIQSVKYIAENMKQAQNEAKEIQDDWKYVA 470
Qy 465 CVVDRCLCMAFSVETIICITIG 485
Db 471 MWIDRIFLW---VFLWCILG 488

Search completed: May 5, 2004, 15:30:30
Job time : 19 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: May 5, 2004, 15:27:17 ; Search time 45 Seconds
(without alignments)
3519.781 Million cell updates/sec

Title: US-09-703-951A-12
Perfect score: 2702
Sequence: 1 MRCSPGGVWLALASLIHVS.....TIGILMSAPNFVAVSKDPA 502

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2679	99.1	502	6 Q866A2	Q866A2 macaca mula
2	2550	94.4	502	11 Q9JHD6	Q9JHD6 mus musculus
3	2077.5	76.9	509	13 Q800C7	Q800C7 brachydanio
4	1849	68.4	513	13 Q7T289	Q7T289 fugu rubrip
5	1820.5	67.4	511	13 Q03481	Q03481 gallus gall
6	1769.5	65.5	486	13 Q7T280	Q7T280 fugu rubrip
7	1734	64.2	555	13 Q7T200	Q7T200 fugu rubrip
8	1705	63.1	321	4 Q8IU24	Q8IU24 homo sapien
9	1575.5	58.3	554	13 Q7T2T9	Q7T2T9 fugu rubrip
10	1569.5	58.1	474	13 Q7T2U1	Q7T2U1 fugu rubrip
11	1271	47.0	542	5 Q86MN7	Q86MN7 drosophila
12	1270.5	47.0	545	5 Q9VW19	Q9VW19 drosophila
13	1264	46.8	807	5 Q87V5	Q87V5 drosophila
14	1258.5	46.6	501	5 Q9XZ14	Q9XZ14 heliothis v
15	1246	46.1	496	5 Q9XZ13	Q9XZ13 heliothis v
16	1225	45.3	494	5 Q87S2	Q87S2 drosophila

17	1223	45.3	494	5	Q8T7S3	Q8T7S3 drosophila
18	1221	45.2	494	5	Q86MN8	Q86MN8 drosophila
19	1218	45.1	494	5	Q8T7S1	Q8T7S1 drosophila
20	1208.5	44.7	509	5	Q8T7S0	Q8T7S0 drosophila
21	1206.5	44.7	523	5	Q8T7R9	Q8T7R9 drosophila
22	1097	40.6	554	5	Q82083	Q82083 caenorhabdi
23	1021.5	37.8	480	5	Q81932	Q81932 caenorhabdi
24	999	37.0	461	5	Q81197	Q81197 caenorhabdi
25	976.5	36.1	523	5	Q46128	Q46128 heliothis v
26	958	35.5	554	5	Q3VL79	Q3VL79 drosophila
27	953.5	35.3	568	5	Q9NFR5	Q9NFR5 drosophila
28	952.5	35.3	545	5	Q96631	Q96631 heliothis v
29	951.5	35.2	536	5	Q8T0Y9	Q8T0Y9 aplysia cal
30	951	35.2	515	5	Q46133	Q46133 locusta mig
31	945	35.0	537	5	Q8MUR0	Q8MUR0 apis mellif
32	945	35.0	542	5	Q18556	Q18556 caenorhabdi
33	943.5	34.9	552	5	Q91765	Q91765 myzus persi
34	942.5	34.9	537	5	Q90941	Q90941 myzus persi
35	942	34.9	505	4	Q86U77	Q86U77 homo sapien
36	941.5	34.8	536	5	Q8T9S0	Q8T9S0 aplysia cal
37	937	34.7	512	11	Q91X60	Q91X60 mus musculu
38	930.5	34.4	520	13	Q7Z2P7	Q7Z2P7 brachydanio
39	924	34.2	795	5	Q18394	Q18394 drosophila
40	922.5	34.1	504	11	Q8BV44	Q8BV44 mus musculu
41	921.5	34.1	499	11	Q8VHH6	Q8VHH6 mus musculu
42	921	34.1	495	11	Q8R493	Q8R493 mus musculu
43	921	34.1	502	5	Q9N587	Q9N587 caenorhabdi
44	920	34.0	439	13	Q7T2S5	Q7T2S5 fugu rubrip
45	919	34.0	540	5	Q46134	Q46134 locusta mig

ALIGNMENTS

RESULT 1

Q866A2 ID Q866A2 PRELIMINARY; PRT; 502 AA.

AC Q866A2; DT 01-JUN-2003 (Tremblrel. 24, Created)

DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE Nicotinic acetylcholine receptor alpha7.

GN CHRNA7.

OS Macaca mulatta (Rhesus macaque).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;

OC Cercopitheciinae; Macaca.

OX NCBI_TaxID=9544;

RN [1]

RP SEQUENCE FROM N.A.

RA Prokocil B.J., Sekhon H.S., Keller J.A., Jia Y., Blakely R.D.,

RA Lindstrom J., Spindel E.R.,

RT "An Intrinsic Non-neuronal Nicotinic Cholinergic Signaling System in

RT Monkey Lung Airway Epithelium,"

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF486623; AA084497.1; -

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0005230; F:extracellular ligand-gated ion channel acti. . .; IEA.

DR GO; GO:0030594; F:neurotransmitter receptor activity; IEA.

DR GO; GO:0006811; P:ion transport; IEA.

DR InterPro; IPR006201; Neur_channel.

DR InterPro; IPR006029; Neur_chan_LBD.

DR Pfam; PF02931; Neur_chan_LBD; 1.

DR Pfam; PF02932; Neur_chan_memb; 1.

DR PRINTS; PR00352; NRIONCHANNEL.

DR TIGRPFAM; TIGR00860; LIC; 1.

DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.

KW Receptor.

SQ SEQUENCE 502 AA; 56429 MW; 213C8A282242AC4A CRC64;

Query Match 99.1%; Score 2679; DB 6; Length 502;

Best Local Similarity 99.0%; Pred. No. 2.9e-229;

	Matches	497; Conservative	3; Mismatches	2; Indels	0; Gaps	0;
QY	1	MRCSPGGVWALAAASLLHVS	LQGEFQRLKYELVNTNPLRPVANDSQPLTVYFS	SL	60	
Db	1	MRCSPGGVWALAAASLLHVS	LQGEFQRLKYELVNTNPLRPVANDSQPLTVYFS	SL	60	
QY	61	QIMDVDEKNQVLTTNIWLQMS	TDHYLQWNVSEYGVKTVFPDGOIKWDPDILLYNSADE	120		
Db	61	QIMDVDEKNQVLTTNIWLQMS	TDHYLQWNVSEYGVKTVFPDGOIKWDPDILLYNSADE	120		
QY	121	RFDATFHTNVLNVS	SGHCQYLPPGPIKSSCCYIDVRVFPFDVQHCKLKFGSGWSYGGWSL	180		
Db	121	RFDATFHTNVLNVS	SGHCQYLPPGPIKSSCCYIDVRVFPFDVQHCKLKFGSGWSYGGWSL	180		
QY	181	QMEADISGYIPNGEWDLVGI	PGKRSRFEYECCKEYPDDVTFTVMRRRTLYYGLNLLIP	240		
Db	181	QMEADISGYIPNGEWDLVGI	PGKRSRFEYECCKEYPDDVTFTVMRRRTLYYGLNLLIP	240		
QY	241	CVLISALALIVFLPAD	SGEKISIGITVLISLTVFMLLVASIMPATSDSVPLIAQYFAST	300		
Db	241	CVLISALALIVFLPAD	SGEKISIGITVLISLTVFMLLVASIMPATSDSVPLIAQYFAST	300		
QY	301	MIIVGLSVVTVTVI	LYQYHHDDPGCGKPKWTRVILLNWCANFLMRKPEBKVPACQHK	360		
Db	301	MIIVGLSVVTVTVI	LYQYHHDDPGCGKPKWTRVILLNWCANFLMRKPEBKVPACQHK	360		
QY	361	QRRCSLASVEMSAVAPP	ASNGLLYTIGFRGLDGVCHVPTPDSGGVVCGRMACSPHTD	420		
Db	361	QRRCSLASVEMSAVAPP	ASNGLLYTIGFRGLDGMHCAPTDPDSGGVVCGRMACSPHTD	420		
QY	421	LHGQPPPEGDPDLAKIL	EEVRYIANRFRQDESAVCSEWKFAACVVDRLCLMAFSVTI	480		
Db	421	LHGQPPPEGDPDLAKIL	EEVRYIANRFRQDESAVCSEWKFAACVVDRLCLMAFSVTI	480		
QY	481	ICTIGILMSAPNFVEAVS	KOFA 502			
Db	481	ICTIGILMSAPNFVEAVS	KOFA 502			

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RESULT 2
Q9JHD6
ID Q9JHD6 PRELIMINARY; PRT; 502 AA.
AC Q9JHD6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Nicotinic acetylcholine receptor subunit alpha 7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;

[1]
RN SEQUENCE FROM N.A.
RP STRAIN=DBA/21bg;
RX MEDLINE=97189245; PubMed=9037516;
RA Stitzel J.A., Farnham D.A., Collins A.C.:
RT "Linkage of strain-specific nicotinic receptor alpha 7 subunit
RT restriction fragment length polymorphisms with levels of alpha-
RT bungarotoxin binding in brain.";
RL Brain Res. Mol. Brain Res. 43:30-40(1996).

[2]
RN SEQUENCE FROM N.A.
RP STRAIN=DBA/21bg;
RA Stitzel J.A.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL; AF225980; AAF35885.1; --
DR MGD; MGI:99779; Chnra7.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005230; F:extracellular ligand-gated ion channel acti. . .; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.

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DR	GO; GO:0030594; F:neurotransmitter receptor activity; IEA.
DR	GO; GO:0006811; P:ion transport; IEA.
DR	GO; GO:0007268; P:synaptic transmission; IEA.
DR	InterPro; IPR006201; Neur_chan_LBD.
DR	InterPro; IPR006202; Neur_chan_LBD.
DR	InterPro; IPR006029; Neu_Channel_memb.
DR	Pfam; PF02931; Neur_chan_LBD; 1_
DR	Pfam; PF02932; Neur_chan_memb; 1.
DR	PRINTS; PR00252; NRIONCHANNEL.
DR	TIGRFAMs; TIGR00860; LIC; 1.
DR	PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
KW	Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
KW	Transmembrane.
SQ	SEQUENCE 502 AA; 56617 MW; C9353E5136D620E3 CRC64;

Query Match	94.4%; Score 2550; DB 11; Length 502;
Best Local Similarity	94.0%; Pred.No. 8.2e-218;
Matches 467; Conservative 19; Mismatches 11; Indels 0; Gaps 0;	

Qy	6	GGVWLALAAALLHVSLSLQGEFRQLYKELVNKNYNPLERPVANDSQPLTVVFSLSLQIMDV	65
Dd	6	GGIWLALAAALLHVSLSLQGEFRRLYKELVNKNYNPLERPVANDSQPLTVVFSLSLQIMDV	65
Qy	66	DEKNQVLTTNIWLQMSVTDHYLVQNWSEYPGVKTVPDPGQIKWKPDILLNYSADDERFAT	125
Dd	66	DEKNQVLTTNIWLQMSVTDHYLVQNMSEYPGVKNVREFPDGQIKWKPDILLNYSADDERFAT	125
Qy	126	FHTNLVNSSGHCQYLPPGIKFSSCYIDVRWFDPDVQHCKLKFGSNWSYGWSDLQMQEA	185
Dd	126	FHTNLVNASGHCCQYLPPGIFKSSCYIDVRWFDPDVQOCKLKFGSNWSYGWSDLQMQEA	185
Qy	186	DISGYIPNGBMDLVGIPGKSRSRYECCKBPYPDVTFTVMRRRTLYYGLNLLIPCWLIS	245
Dd	186	DISSYIPNGBMDLMGIPGKNEKYECKBPYPDVTFTVMRRRTLYYGLNLLIPCWLIS	245
Qy	246	ALALLVELLPADSGEKISLGITVLLSTVFMILVAETMPATSDSVPLIAOYFASTMIIVG	305
Dd	246	ALALLVELLPADSGEKISLGITVLLSTVFMILVAETMPATSDSVPLIAOYFASTMIIVG	305
Qy	306	LSVVTVTIVLQYHHHPDGGMKPQKWTRVILLINWCANFLMRKPGEDKVRPACQHKQRCS	365
Dd	306	LSVVTVTIVLRYYHHPDGGMKPQKWTRIILLINWCANFLMRKPGEDKVRPACQHKPRCS	365
Qy	366	LASVEMSAVAPPASNGLIYIGRGLDGVCHVTPDSGVVCGRMACSPTHDEHLHGQG	425
Dd	366	LASVELSAGAPPPSSGNGLIYIGRGLEGMHCAFTPDSGVVCGRIACSPTHDEHMGHGT	425
Qy	426	PPEGDPDLAKILEEVRIYIANFRQCDSEASEVCSEWKAACVVDRLCLMAFSVFTICTIG	485
Dd	426	PSGDGPDLAKILEEVRIYIANFRQCDSEVICSEWKAACVVDRLCLMAFSVFTICTIG	485
Qy	486	ILMSAPNFVEAVSKDFA 502	
Dd	486	ILMSAPNFVEAVSKDFA 502	

RESULT 3	
Q800C7	PRELIMINARY; PRT; 509 AA.
ID	Q800C7
AC	Q800C7; TREMBLrel. 24, Created)
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT	01-JUN-2003 (TREMBLrel. 25, Last annotation update)
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE	Nicotinic acetylcholine receptor alpha 7 subunit.
OS	Brachydanio rerio (zebrafish) (Danio rerio).
OC	Eukaryota; Metazoa (Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC	Cyprinidae; Danio.
OX	NCBI_TaxID=7955;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Zigter J.M., Boyd R.T.;
RT	"Cloning and expression of zebrafish neuronal nicotinic acetylcholine


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RL Neuron 5:35-48(1990).
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL: X52296; CAA36544.1; -.
DR PIR: JH0173; JH0173.
DR GO: GO:0016021; C:intrigral to membrane; IEA.
DR GO: GO:0005230; F:extracellular ligand-gated ion channel acti. .; IEA.
DR GO: GO:0005216; F:ion channel activity; IEA.
DR GO: GO:0030594; F:neurotransmitter receptor activity; IEA.
DR GO: GO:0006811; P:ion transport; IEA.
DR GO: GO:0007268; P:synaptic transmission; IEA.
DR InterPro: IPR006201; Neur channel.
DR InterPro: IPR006202; Neur channel.
DR InterPro: IPR006029; Neu channel memb.
DR Pfam: PF02931; Neur chan LBD; 1.
DR Pfam: PF02932; Neur chan memb; 1.
DR PRINTS: PR00252; NRIONCHANNEL.
DR TIGSFams: TIGR00860; LIC; 1.
DR PROSITE: PS00236; NEUROTR ION CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor; Signal; Transmembrane.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 511 POTENTIAL.
SQ SEQUENCE 511 AA; 58705 MW; 10F362D153EC87A7 CRC64;

Query Match 67.4%; Score 1820.5; DB 13; Length 511;
Best Local Similarity 69.0%; Pred. No. 5.4e-153;
Matches 343; Conservative 56; Mismatches 93; Indels 5; Gaps 4;

QY 8 VMLAASLLHSLQGEFQKLYKELVKNYPLRPVANDSQPLTYFSLSLQIMDVE 67
DB 16 LNASLFLSPFKYSQQGSQRRLYDLRLNRYNLERPWNDSQPIVVELQLLQIDVDE 75
QY 68 KQVLTNTNLQMSWDHYLQWNVSEYPGVKTRPDPDGOIKWPKDILLYNSADERFADPH 127
DB 76 KQVLTITNLQWYVDIYLSWDQYEPGVQNLRFPSDQIWPDIILYNSADERFADPH 135
QY 128 TNLVNSSGHCOYLPGIPFKSSCYIDVRWFPDQVHCKLKFGWSYSGWLSLQMOEADI 187
DB 136 TNLVNYSGCOYIPPGILKSTCYIDVRWFPDQVHCKLKFGSWTHSGWLDLQMLEADI 195
QY 188 SGVINGEWDLVGIGKRSERFECKEYDPDVTFTVTRRTLYYGLNLLIPCVLISAL 247
DB 196 SVYISNGEWDLVGVPGRNELYECKEYDPDVTFTVTRRTLYYGLNLLIPCVLISGL 255
QY 248 ALLVFLPADSGEKISLGITVLLSLTFVLLVAEIMPATSDSVPLIAQYFASTMIIVGLS 307
DB 256 ALLVFLPADSGEKISLGITVLLSLTFVLLVAEIMPATSDSVPLIAQYFASIMVIGLS 315
QY 308 VVVTVIVLQYHHDDPGGKMPKWRVILLNWCWFLRMKRPGEKVRP-ACQHK--QRRC 364
DB 316 VVVTVIVLQYHHDDPGGKMPKWRVILLNWCWFLRMKRPGEKVRP-ACQHK--QRRC 374
QY 365 SLASVEMSAVAPPASGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPHDEHLHGG 424
DB 375 SLKNTENVLPQHSNGNIY-SYHTMENPCQNNIDGSGKICPLSDENHEVQKK 433
QY 425 QPGEQDPLAKILEEVRYIANFRQDSEAVCSWKFAACVVDRLCLMAFSVFTIICIT 484
DB 434 ALMDTIPVIVKILEEVQYFAMFRKQDEGEIEICSEWKFAAAVVDRLCLVAFVFLAICT 493
QY 485 GILMSAPNFEAVSKDF 501
DB 494 TILMSAPNFEAVSKDF 510

RESULT 6
QYT2S0 PRELIMINARY; PRT; 486 AA.
AC QYT2S0;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

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DE Nicotinic acetylcholine receptor alpha 8a subunit (Fragment).
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]_TaxID=31033;
RP SEQUENCE FROM N.A.
RA Jones A.K., Elgar G., Sattelle D.B.;
RT "The nicotinic acetylcholine receptor gene family of the pufferfish,
RT Fugu rubripes."
RL Genomics 0:0-0(2003).
DR EMBL: AY299465; AAP58380.1; -.
KW Receptor.
FT NON_TER 1 1
SQ SEQUENCE 486 AA; 54942 MW; D27198395A87A4A CRC64;

Query Match 65.5%; Score 1769.5; DB 13; Length 486;
Best Local Similarity 68.6%; Pred. No. 1.7e-148;
Matches 338; Conservative 48; Mismatches 82; Indels 25; Gaps 6;

QY 23 GEFQKLYKELVKNYPLRPVANDSQPLTYFSLSLQIMDVEKQVLTNTNLQMSW 82
DB 4 GPFQKLYHDLNMYNRYNLERPVLNDSAPIVVELGFTLQIIVDEKQVLTNTNLQMSW 63
QY 83 TDHYLQWNVSEYPGVKTRPDPDGOIKWPKDILLYNSADERFADPHVNVNSSGHCOYLP 142
DB 64 TDYLSWNPESFPQVQNLRFPSLIMWPDILLYNSADERFADPHVNVNATGVCQYIP 123
QY 143 GPFKSSCYIDVRWFPDQVHCKLKFGWSYSGWLSLQMOEADISGYPNGEWDLVGP 202
DB 124 GPILKSTCYIDVRWFPDQVHCKLKFGSWTHGWLDDIQQMDVDISTYIPNGEWDLVGP 183
QY 203 GKRSERFECKEYDPDVTFTVTRRTLYYGLNLLIPCVLISALALLVFLPADSGEKI 262
DB 184 AKRNLVYDCKEYDPDVTFTVTRRTLYYGLNLLIPCVLISGLALLVFLPADSGEKI 243
QY 263 SLGITVLLSLTFVLLVAEIMPATSDSVPLIAQYFASTMIIVGLSVVTVIVLQYHHDP 322
DB 244 SLGITVLLSLTFVLLVAEIMPATSDSVPLIAQYFASTMIIVGLSVVTVIVLQYHHDP 303
QY 323 DGGKMPKWRVILLNWCWFLRMKRPGEKVRPAC-----QHKRRCSLASVEMSAV 374
DB 304 HGGKMPKWRVILLNWCWFLRMKRPGEKQVASSRPPDHKRSPPHASSASTIQVATI 363
QY 375 ---APPPASGNL-LYIGR--GLDGVHCVPTPDSGVVCGRMACSPHDEHLHGGQPP 428
DB 364 PQQAPAPTANGNNLLYFSYHALADNPTLPASDPVSIRSRQTRS-----LL-----LE 412
QY 429 GDPDLAKILEEVRYIANFRQDSEAVCSWKFAACVVDRLCLMAFSVFTIICITILM 488
DB 413 QLPEISQILEEVQYIARFRQDSEAVCSWKFAACVVDRLCLVAFVFLAICTFTILM 472
QY 489 SAPNFEAVSKDF 501
DB 473 SAPNFEAVSKDF 485

RESULT 7
QYT2U0 PRELIMINARY; PRT; 555 AA.
AC QYT2U0;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Nicotinic acetylcholine receptor alpha 7b subunit (Fragment).
GN A7B.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.

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OX NCBI_TaxID=31033;
RN SEQUENCE FROM N.A.
RA Jones A.K., Elgar G., Sattelle D.B.;
RT "The nicotinic acetylcholine receptor gene family of the pufferfish,
RL Fugu rubripes.";
RT Genomics 0:0-0(2003).
DR EMBL; AY298752; AAP57216.1; -.
KW Receptor.
FT NON TER
SQ SEQUENCE 555 AA; 61010 MW; B042A3E4430A2B7C CRC64;

Query Match      64.2%; Score 1734; DB 13; Length 555;
Best Local Similarity 60.8%; Pred. No. 2.9e-145;
Matches 337; Conservative 52; Mismatches 93; Indels 72; Gaps 6;

QY 20 SLQGEFORKLYKEIVKYNPLERVANDSOPLTVYFSLQLQIMVDEKQVLTNTWLQ 79
DQ 1 SLQGEFORKLYKEIVKYNPLERVANDSOPLTVYFSLQLQIMVDEKQVLTNTWLQ 79
DQ 1 SLQGEFORKLYKEIVKYNPLERVANDSOPLTVYFSLQLQIMVDEKQVLTNTWLQ 79
QY 80 MSWTDHYLQNVSEYGVKTVRFDPGQIKWPKDILLVNSADDERFDTHTNVLNNSGHQ 139
DQ 1 MSWTDHYLQNVSEYGVKTVRFDPGQIKWPKDILLVNSADDERFDTHTNVLNNSGHQ 139
DQ 1 MSWTDHYLQNVSEYGVKTVRFDPGQIKWPKDILLVNSADDERFDTHTNVLNNSGHQ 139
QY 140 YLPPGIKSSCYIDVRFPEDVQCKLKFGSWYGGWSLDLQMQEADISGYIPNGEWDLV 199
DQ 1 YLPPGIKSSCYIDVRFPEDVQCKLKFGSWYGGWSLDLQMQEADISGYIPNGEWDLV 199
DQ 1 YLPPGIKSSCYIDVRFPEDVQCKLKFGSWYGGWSLDLQMQEADISGYIPNGEWDLV 199
QY 121 YQPPGIEMSTCNVDRFPEDVQCKLKFGSWYGGWSLDLQMQEADISGYIPNGEWDLV 180
DQ 1 YQPPGIEMSTCNVDRFPEDVQCKLKFGSWYGGWSLDLQMQEADISGYIPNGEWDLV 180
DQ 1 YQPPGIEMSTCNVDRFPEDVQCKLKFGSWYGGWSLDLQMQEADISGYIPNGEWDLV 180
QY 200 GIFPKRSERFECCKEYPDVFTVIMRRRTLYYGLNLLIPCVLISALALLVFLPADSG 259
DQ 1 GIFPKRSERFECCKEYPDVFTVIMRRRTLYYGLNLLIPCVLISALALLVFLPADSG 259
DQ 1 GIFPKRSERFECCKEYPDVFTVIMRRRTLYYGLNLLIPCVLISALALLVFLPADSG 259
QY 181 GVPQTRNEVFYDCKEYPDVFTVIMRRRTLYYGLNLLIPCVLISALALLVFLPADSG 240
DQ 1 GVPQTRNEVFYDCKEYPDVFTVIMRRRTLYYGLNLLIPCVLISALALLVFLPADSG 240
DQ 1 GVPQTRNEVFYDCKEYPDVFTVIMRRRTLYYGLNLLIPCVLISALALLVFLPADSG 240
QY 260 EKISLGLTVLISLTVFLLVAEIMPATSDSVPLIAQYFASMTIIVGLSVVTVVLQYHH 319
DQ 1 EKISLGLTVLISLTVFLLVAEIMPATSDSVPLIAQYFASMTIIVGLSVVTVVLQYHH 319
DQ 1 EKISLGLTVLISLTVFLLVAEIMPATSDSVPLIAQYFASMTIIVGLSVVTVVLQYHH 319
QY 241 EKISLGLTVLISLTVFLLVAEIMPATSDSVPLIAQYFASMTIIVGLSVVTVVLQYHH 300
DQ 1 EKISLGLTVLISLTVFLLVAEIMPATSDSVPLIAQYFASMTIIVGLSVVTVVLQYHH 300
DQ 1 EKISLGLTVLISLTVFLLVAEIMPATSDSVPLIAQYFASMTIIVGLSVVTVVLQYHH 300
QY 320 HDPDGGMKPKWTRVILLNCAWFLMKRPGCE--DKVPAQCHQKRRCSLASEVMSAVPP 377
DQ 1 HDPDGGMKPKWTRVILLNCAWFLMKRPGCE--DKVPAQCHQKRRCSLASEVMSAVPP 377
DQ 1 HDPDGGMKPKWTRVILLNCAWFLMKRPGCE--DKVPAQCHQKRRCSLASEVMSAVPP 377
QY 301 HDPNGMNPQWVQLVQLQWAVFLMKRPGCEKSPERPPCAPHLRCSGSGSGSINPPF 360
DQ 1 HDPNGMNPQWVQLVQLQWAVFLMKRPGCEKSPERPPCAPHLRCSGSGSGSINPPF 360
DQ 1 HDPNGMNPQWVQLVQLQWAVFLMKRPGCEKSPERPPCAPHLRCSGSGSGSINPPF 360
QY 378 -----PASNGNLLYIGFRLDGVHCVPTPDSDGVVCGMACSPTHDHL 403
DQ 1 -----PASNGNLLYIGFRLDGVHCVPTPDSDGVVCGMACSPTHDHL 403
DQ 1 -----PASNGNLLYIGFRLDGVHCVPTPDSDGVVCGMACSPTHDHL 403
QY 361 DHALHPLHPQGLAPLQGLHAGQPHVHAQSSANNNGNLVILGFQSVDSAGLPEIQRN 420
DQ 1 DHALHPLHPQGLAPLQGLHAGQPHVHAQSSANNNGNLVILGFQSVDSAGLPEIQRN 420
DQ 1 DHALHPLHPQGLAPLQGLHAGQPHVHAQSSANNNGNLVILGFQSVDSAGLPEIQRN 420
QY 404 GVVCG--RMACS-PTHDEHLLHGQPPE----- 428
DQ 1 GVVCG--RMACS-PTHDEHLLHGQPPE----- 428
DQ 1 GVVCG--RMACS-PTHDEHLLHGQPPE----- 428
QY 421 NISTGPRVAGSPPHLPQSCSPPPASNMMDTGCPSITVSSGGGFGGGGGLGCSASA 480
DQ 1 NISTGPRVAGSPPHLPQSCSPPPASNMMDTGCPSITVSSGGGFGGGGGLGCSASA 480
DQ 1 NISTGPRVAGSPPHLPQSCSPPPASNMMDTGCPSITVSSGGGFGGGGGLGCSASA 480
QY 429 -GPDPLAKILLEEVRYIANRFRQDESEAVSEWKFACVVDRLCLMAFSVFTIIGIL 487
DQ 1 -GPDPLAKILLEEVRYIANRFRQDESEAVSEWKFACVVDRLCLMAFSVFTIIGIL 487
DQ 1 -GPDPLAKILLEEVRYIANRFRQDESEAVSEWKFACVVDRLCLMAFSVFTIIGIL 487
QY 481 VGDPLHALLEEVRYIANRFRQDESEAVSEWKFACVVDRLCLMAFSVFTIIGIL 540
DQ 1 VGDPLHALLEEVRYIANRFRQDESEAVSEWKFACVVDRLCLMAFSVFTIIGIL 540
DQ 1 VGDPLHALLEEVRYIANRFRQDESEAVSEWKFACVVDRLCLMAFSVFTIIGIL 540
QY 488 MSAPNFVEAVSKDF 501
DQ 1 MSAPNFVEAVSKDF 501
DQ 1 MSAPNFVEAVSKDF 501
QY 541 MSAPNFVEAVSKDF 554
DQ 1 MSAPNFVEAVSKDF 554
DQ 1 MSAPNFVEAVSKDF 554

RESULT 8
Q8IU24 PRELIMINARY; PRT; 321 AA.
AC Q8IU24;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN SEQUENCE FROM N.A.
RP Jones A.K., Elgar G., Sattelle D.B.;
RC "The nicotinic acetylcholine receptor gene family of the pufferfish,
RA Fugu rubripes.";
RA Genomics 0:0-0(2003).
RA EMBL; AY298752; AAP57216.1; -.
RA Receptor.
RA NON TER
RA SEQUENCE 555 AA; 61010 MW; B042A3E4430A2B7C CRC64;

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RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC037571; AAH37571.1; -.
DR GO; GO:0016020; C:membranes; IEA.
DR GO; GO:0005230; F:extracellular ligand-gated ion channel acti.; IEA.
DR GO; GO:0030594; F:neurotransmitter receptor activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR InterPro; IPR006201; Neur_chan.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006029; Neur_chan_memb.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR TIGRFAMs; TIGR00860; LiC; 1.
DR Hypothetical protein.
SQ SEQUENCE 321 AA; 35481 MW; 2998C11DD1F15A89 CRC64;

Query Match      63.1%; Score 1705; DB 4; Length 321;
Best Local Similarity 100.0%; Pred. No. 5.4e-143;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 182 MQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVFTVIMRRRTLYYGLNLLIP 241
DQ 1 MQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVFTVIMRRRTLYYGLNLLIP 241
DQ 1 MQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVFTVIMRRRTLYYGLNLLIP 241
QY 242 VLISALALLVFLPADSGEKISLGLTVLISLTVFLLVAEIMPATSDSVPLIAQYFASMT 301
DQ 1 VLISALALLVFLPADSGEKISLGLTVLISLTVFLLVAEIMPATSDSVPLIAQYFASMT 301
DQ 1 VLISALALLVFLPADSGEKISLGLTVLISLTVFLLVAEIMPATSDSVPLIAQYFASMT 301
QY 302 IIVGLSVVTVVLQVHHHDPDGKMPKTRVILLNCAWFLMKRPGEDKVPACQHKQ 361
DQ 1 IIVGLSVVTVVLQVHHHDPDGKMPKTRVILLNCAWFLMKRPGEDKVPACQHKQ 361
DQ 1 IIVGLSVVTVVLQVHHHDPDGKMPKTRVILLNCAWFLMKRPGEDKVPACQHKQ 361
QY 362 RRCSLASVMSAVAPPASNGNLLYIGFRLDGVHCVPTPDSDGVVCGMACSPTHDHL 421
DQ 1 RRCSLASVMSAVAPPASNGNLLYIGFRLDGVHCVPTPDSDGVVCGMACSPTHDHL 421
DQ 1 RRCSLASVMSAVAPPASNGNLLYIGFRLDGVHCVPTPDSDGVVCGMACSPTHDHL 421
QY 422 HGQOPGEGDPLAKILLEEVRYIANRFRQDESEAVSEWKFACVVDRLCLMAFSVFTII 481
DQ 1 HGQOPGEGDPLAKILLEEVRYIANRFRQDESEAVSEWKFACVVDRLCLMAFSVFTII 481
DQ 1 HGQOPGEGDPLAKILLEEVRYIANRFRQDESEAVSEWKFACVVDRLCLMAFSVFTII 481
QY 482 CTIGILMSAPNFVEAVSKDFA 502
DQ 1 CTIGILMSAPNFVEAVSKDFA 502
DQ 1 CTIGILMSAPNFVEAVSKDFA 502

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```

RESULT 9
Q7T2T9 PRELIMINARY; PRT; 554 AA.
AC Q7T2T9;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Nicotinic acetylcholine receptor alpha 7c subunit (Fragment).
GN A7C.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN SEQUENCE FROM N.A.
RP Jones A.K., Elgar G., Sattelle D.B.;
RT "The nicotinic acetylcholine receptor gene family of the pufferfish,
RL Fugu rubripes.";
RL Genomics 0:0-0(2003).
DR EMBL; AY298753; AAP57217.1; -.
KW Receptor.
FT NON TER
SQ SEQUENCE 554 AA; 61565 MW; 8C46BCC6B20B5AFB CRC64;

Query Match      58.3%; Score 1575.5; DB 13; Length 554;
Best Local Similarity 55.7%; Pred. No. 3.5e-131;
Matches 309; Conservative 68; Mismatches 103; Indels 75; Gaps 8;

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QY 20 SLOGEFORKLYKELVKNYNPLERPVANDSOPLTIVYFSLSLQIMDVDEKQVLTINWLQ 79
Db 1 SVQGPQORFELLTELLKDYNEPWPVANDSQAIVTQFSFILIQVMDVDEKQVLTINWLQ 60
QY 80 MSWTDHYLQWNVSEYFGVKTVPDPGQIWKPDILLNYSADERPDATHTNVLVNSGHCQ 139
Db 61 MOWTDHYLQWNVSEYFGVKTVPDPGQIWKPDILLNYSADERPDATHTNVLVNSGHCQ 120
QY 140 YLPPGIFKSCYIDVRNFPFQVCHCKLKFGSWYSGWSDLQMOEADISGYIPNGEWDLV 199
Db 121 YLPPGIFKSCYIDVRNFPFQVCHCKLKFGSWYSGWSDLQMOEADISGYIPNGEWDLV 180
QY 200 GIFKKSERYECCKEBPYDVTFTVTMMRRRTLYYGLNLLIPCVLISALALLVFLPADSG 259
Db 181 EYVGGREHEFYDCCABEPYDVTFTVTMMRRRTLYYGLNLLIPCVLISALALLVFLPADSG 240
QY 260 EKISLGIITVLLSTVFMMLVAEIMPATSDSVPLIAQYFASTMIIVGLSVVTVIVLYYHH 319
Db 241 EKISLGIITVLLSTVFMMLVAEIMPATSDSVPLIAQYFASTMIIVGLSVVTVIVLYYHH 300
QY 320 HDPDGGKMPKTRVILLNWCAMFLRMKRPGEOKVRPACQHKQ-----RRCS-----LASVE 370
Db 301 HNTNNGQMPRWHLVLLQWIPFLRMKHPGETB-EPSSLPHSQTSASOKLSSEGTSSSS 359
QY 371 MSNVAPEPPAS-----NGMLLYIGFRGLDGVHCVPTPDGSGVVCGRMAC- 412
Db 360 SSSAAARPAANTDQGLSLRQLRQSLNGALYVGFQATAPR-EPQSRSVSNRVRGCG 418
QY 413 -----SPTHDEHLL-----HGG--QP 426
Db 419 DGEAGASVERGSPSLVQRLPLSLKSEVPQLEGTPGPDASSGSGGAEPHPPGGLTQS 478
QY 427 PEGDPLAKILEVRYIANFRQDSEAVCSWKFAACVVDRLCLMAFSVFTHICTIGI 486
Db 479 PVVRQQLQALLAEVQFLVERVKQDRQLRLAEQWQFAASVIDRLFLVGSVFVNICTIAI 538
QY 487 LMSAPNFVAVSKDF 501
Db 539 LMAAPHFGALSXDF 553

RESULT 10
Q7T2U1 ID Q7T2U1 PRELIMINARY; PRT; 474 AA.
AC Q7T2U1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Nicotinic acetylcholine receptor alpha 7a subunit (Fragment).
GN A7A.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
SEQUENCE FROM N.A.
RA Jones A.K., Elgar G., Sattelle D.B.;
RT "The nicotinic acetylcholine receptor gene family of the pufferfish,
RT Fugu rubripes."
RL Genomics 0:0-0(2003).
DR EMBL; AY298751; AAF57215.1; -.
KW Receptor.
FT NON TER
SQ SEQUENCE 474 AA; 53180 MW; 9843B897C8D505FD CRC64;

Query Match 58.1%; Score 1569.5; DB 13; Length 474;
Best Local Similarity 63.1%; Pred. No. 9.6e-131;
Matches 306; Conservative 64; Mismatches 100; Indels 15; Gaps 5;

QY 20 SLOGEFORKLYKELVKNYNPLERPVANDSOPLTIVYFSLSLQIMDVDEKQVLTINWLQ 79

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Db 1 TVQGPTEERLYNLLRRYNSMIRPVANDSETLMVRLGLSLQIMDVDEKQVLTINWLQ 60
QY 80 MSWTDHYLQWNVSEYFGVKTVPDPGQIWKPDILLNYSADERPDATHTNVLVNSGHCQ 139
Db 61 MOWTDHYLQWNVSEYFGVKTVPDPGQIWKPDILLNYSADERPDATHTNVLVNSGHCQ 120
QY 140 YLPPGIFKSCYIDVRNFPFQVCHCKLKFGSWYSGWSDLQMOEADISGYIPNGEWDLV 199
Db 121 YLPPGIFKSCYIDVRNFPFQVCHCKLKFGSWYSGWSDLQMOEADISGYIPNGEWDLV 180
QY 200 GIFKKSERYECCKEBPYDVTFTVTMMRRRTLYYGLNLLIPCVLISALALLVFLPADSG 259
Db 181 EYVGGREHEFYDCCABEPYDVTFTVTMMRRRTLYYGLNLLIPCVLISALALLVFLPADSG 240
QY 260 EKISLGIITVLLSTVFMMLVAEIMPATSDSVPLIAQYFASTMIIVGLSVVTVIVLYYHH 319
Db 241 EKISLGIITVLLSTVFMMLVAEIMPATSDSVPLIAQYFASTMIIVGLSVVTVIVLYYHH 300
QY 320 HDPDGGKMPKTRVILLNWCAMFLRMKRPGEOKVRPACQHKQ-----RRCS-----LASVE 379
Db 301 HDPDGGKMPKTRVILLNWCAMFLRMKRPGEOKVRPACQHKQ-----RRCS-----LASVE 359
QY 380 SGNLLYIGFRGLDGVHCVPTPDGSGVVCGRMACSPHDEHLLHGGQPPGEG---DPLAKI 436
Db 360 PTN--VYPSISGLKS-----SQTTPVPGGRAG---EDELAKGPGSSAGNIERELAKL 408
QY 437 LEEVRYIANFRQDSEAVCSWKFAACVVDRLCLMAFSVFTHICTIGILMSAPNFVAV 496
Db 409 LEEVRYIANFRQDSEAVCSWKFAACVVDRLCLMAFSVFTHICTIGILMSAPNFVAV 468
QY 497 VSKDF 501
Db 469 FSKNF 473

RESULT 11
Q86MN7 ID Q86MN7 PRELIMINARY; PRT; 542 AA.
AC Q86MN7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Nicotinic acetylcholine receptor subunit Dalpha7 precursor.
GN NACRALPHA-18C.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
SEQUENCE FROM N.A.
RA Millar N.S.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ554210; CAD86936.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005230; F:extracellular ligand-gated ion channel acti...; IEA.
DR GO; GO:0030594; F:neurotransmitter receptor activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR InterPro; IPR006201; Neur_chan.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006029; Neur_chan_memb.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Signal; Receptor.
FT SIGNAL
FT CHAIN 36 542
FT CHAIN 36 542
SQ SEQUENCE 542 AA; 60988 MW; 69D2C39746BB74D7 CRC64;

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Query Match 47.0%; Score 1271; DB 5; Length 542;
Best Local Similarity 46.8%; Pred. No. 3.8e-103;
Matches 252; Conservative 87; Mismatches 133; Indels 66; Gaps 8;

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QY 6 GGVWLAALASLL---HVSLOGEFOFKLYKLVKNVNLPRVANDSQPLTYVESLSLQI 62
DB 16 GGRMLVYGLGLIMIPACAGPHEKRLHLDNVSILPRPVNESDPLQFSLTLMQI 75
QY 63 MDVDEKQVLTNTIWLQMSWTDHYLQNVSVYPGVKTVFPDGGQIKWPKDILLNSADERY 122
DB 76 IDVDKQQLITNTIWLKLEWMDNLRWNSSEFGVDRDIRIPHLKPKDVLWNSADEGF 135
QY 123 DATHTNTLVNNSGHCQVLPKIKSSCYIDVRFPDVOQCKLFGWSVGGWSLIDQM 182
DB 136 DGTATNVNVRNNSCLVVPFGIFKSTCKIDITWFPDQDQRCMKFGSTWYDGFQDLQL 195
QY 183 QE---ADISYIPNGEWDLVGIPGKRSERFYECCKEPPDVTFTVWRRRTLYYGLNLI 239
DB 196 QDEAGGDISSFITNGEWDLVGPGKNEIYVNCPEYIDITFAILLIRKLYYFFNLIV 255
QY 240 PCVLISALALLVFLPADSGKISIGITVLSLTFVLMVAEIMPATSDSVPLIAQYFAS 299
DB 256 PCVLIASMALLGFTLPDPSGKLSIGVTLISLTFVLMVAETPATSDAVPLLGKYFNC 315
QY 300 TMIIVGLSVVTVLVLOVHHDDPGKMPKWTIRVILLNWCANFLMRKPG----- 349
DB 316 IMFVASSVSTILVLYHNRNPDTHSEWIRVIFLWPCILMRQRPQGVYECPPPP 375
QY 350 -----EKVIPA-----COHKQRCSLASVMSAVAP 376
DB 376 SSSSSASGKKQIQNVELKERSKSLANLVLDIDDDFCNH---RCA-----SATLP 426
QY 377 PPASGNLLYIGFGLDGHVCPPTDGSVGVGRMACSPTDHEHLHGGQPEGDPDLAKI 436
DB 427 HQPTYTYRTMY---RQGDGSGVPGVPGVVDGRL-----HEATSHCLTSSABVELALI 478
QY 437 LEEVRYIANFRCDSEAEVSEWKEACVVDRLCLMAFSVFTTICITIGILMSAPNV 494
DB 479 LKELRWTEQLKREDETSIDTRDKFAAMVVDRLCLIFTLTITLTIATLAVLFSAPHF 536
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RESULT 12

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Q9VW19 PRELIMINARY; PRT; 545 AA.
AC Q9VW19;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CG32538 protein.
GN NACR-ALPHA-18C OR CG8082 OR CG8109 OR CG32538.
OS Drosophila melanogaster (Fruit fly).
OC Neoptera; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.P., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.N., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman B., Carlson J.W., Celniker S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RA "Annotation of Drosophila melanogaster genome";
RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[5]
RP SEQUENCE FROM N.A.
RA FlyBase;
RN Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
EMBL; AE003511; AAF48950.2; -.
DR FlyBase; FBgn0031014; nACR-alpha-18C.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005230; F:extracellular ligand-gated ion channel acti. .; IEA.
DR GO; GO:0030594; F:neurotransmitter receptor activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR InterPro; IPR006201; Neur channel.
DR InterPro; IPR006202; Neur chan IBD.
DR InterPro; IPR006029; Neu_chan_LED; 1_memb.
DR Pfam; PF02931; Neur_chan_LED; 1_memb.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
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Wed May 12 09:51:15 2004

us-09-703-951a-12.rspt

Page 10

Db 453 DADISRWKPEAMVDRCLLIIFTLETTIATLAVLLSAPHIM 494

Search completed: May 5, 2004, 15:31:29
Job time : 48 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 5, 2004, 15:27:53 ; Search time 21 Seconds
(without alignments)
2299.436 Million cell updates/sec

Title: US-09-703-951A-12
Perfect score: 2702
Sequence: 1 MRCSPGGVWLAASLLHVS.....TIGILMSAPNFVBAVSKDFA 502

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78:**

1: Piri:**

2: Piri:**

3: Piri:**

4: Piri:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2694	99.7	502	1	ACHUA7
2	2694	99.7	502	2	nicotinic acetylch alpha 7 neuronal n
3	2549	94.3	502	2	nicotinic acetylch
4	2535	93.8	502	2	nicotinic receptor
5	2433	90.0	502	2	nicotinic acetylch
6	1820.5	67.4	511	2	nicotinic acetylch
7	1108.5	41.0	498	2	alpha-bungarotoxin
8	1093.5	40.5	560	2	nicotinic acetylch
9	999	37.0	461	2	hypothetical prote
10	949	35.1	557	2	hypothetical prote
11	946.5	35.0	511	2	nicotinic acetylch
12	945	35.0	542	2	nicotinic acetylch
13	942.5	34.9	459	2	hypothetical prote
14	941.5	34.8	528	1	nicotinic acetylch
15	940.5	34.8	503	2	nicotinic acetylch
16	938	34.7	622	1	nicotinic acetylch
17	937.5	34.7	576	1	nicotinic acetylch
18	937	34.7	502	2	nicotinic acetylch
19	926	34.3	567	1	nicotinic acetylch
20	920	34.0	627	2	nicotinic acetylch
21	919.5	34.0	495	2	nicotinic acetylch
22	917.5	34.0	625	2	acetylcholine rece
23	913	33.8	495	2	nicotinic acetylch
24	902	33.4	494	2	nicotinic acetylch
25	896	33.2	517	2	probable nicotinic
26	891.5	33.0	499	2	nicotinic acetylch
27	885	32.8	498	2	nicotinic acetylch
28	881	32.6	521	1	nicotinic acetylch
29	880.5	32.6	491	1	nicotinic acetylch

ALIGNMENTS

RESULT 1

ACHUA7

Nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - human
N/Alternate names: cholinergic nicotinate receptor alpha-7 chain
C/Species: Homo sapiens (man)
C/Date: 12-Aug-1996 #sequence revision 31-Jan-1997 #text_change 22-Jun-1999
C/Accession: I37185; A54194; S60309

R/Peng, X.; Katz, M.; Gerzanich, V.; Anand, R.; Lindstrom, J.

Mol. Pharmacol. 45, 546-554, 1994

A/Title: Human alpha 7 acetylcholine receptor: cloning of the alpha 7 subunit from the

omers expressed in Xenopus oocytes.

A/Reference number: I37185; MUID:94195283; PMID:8145738

A/Accession: I37185

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-502 <PEN>

A/Cross-references: EMBL:X70297; NID:g496606; PIDN:CAA49778.1; PID:g496607

A/Experimental source: brain neuroblastoma cell line SHSY-5Y

R/Chini, B.; Raimond, E.; Elgoyhen, A.B.; Moralli, D.; Balzaret, M.; Heinemann, S.

Genomics 19, 379-381, 1994

A/Title: Molecular cloning and chromosomal localization of the human alpha-7-nicotinic

A/Reference number: A54194; MUID:94245214; PMID:8188270

A/Accession: A54194

A/Molecule type: mRNA

A/Residues: 24-363, 'S', '365-374, 'A', '376-408, 'AWPAP', 414-502 <CHI>

A/Cross-references: GB:Z23141; NID:g457736; PIDN:CAA80672.1; PID:g457737

A/Experimental source: retina

C/Comment: This acetylcholine receptor is blocked by alpha-bungarotoxin and is localiz

C/Genetics:

A/Gene: GDB:CHRNA7

A/Cross-references: GDB:138751; OMIM:118511

A/Map position: 15q14-15q14

A/Note: defects in this gene have been associated with mental retardation and schizop

C/Complex: the functional receptor molecule is a heteropentamer with two alpha chains

C/Superfamily: acetylcholine receptor

F/1-23/Domain: signal sequence #status predicted <SIG>

F/24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status pre

F/231-254/Domain: transmembrane #status predicted <TR1>

F/262-280/Domain: transmembrane #status predicted <TR2>

F/296-317/Domain: transmembrane #status predicted <TR3>

F/470-488/Domain: transmembrane #status predicted <TR4>

F/46,90,133/Binding site: carbohydrate (Asn) (covalent) #status predicted

F/150-164/Disulfide bonds: #status predicted

F/365,413/Binding site: phosphate (Ser) (covalent) #status predicted

F/415/Binding site: phosphate (Thr) (covalent) #status predicted

F/442/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match

Best Local Similarity 99.7%; Score 2694; DB 1; Length 502;

Matches 500; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAALASLLHVSLOGEFQRLKYLKYNPLERPVANDSQPLTVYFSLIL 60
 DB 1 MRCSPGGVWLAALASLLHVSLOGEFQRLKYLKYNPLERPVANDSQPLTVYFSLIL 60
 QY 61 QIMDVDEKNOVLTTNIWLQMSWDHYLQWNVSEYGVKTVRPDQGIWKPDIILLNSADE 120
 DB 61 QIMDVDEKNOVLTTNIWLQMSWDHYLQWNVSEYGVKTVRPDQGIWKPDIILLNSADE 120
 QY 121 RFDAFHTNVLVNSGHCQYLPPGIFKSSCYIDVRWFFPDVQCHCKLKFGSWYGGWSL 180
 DB 121 RFDAFHTNVLVNSGHCQYLPPGIFKSSCYIDVRWFFPDVQCHCKLKFGSWYGGWSL 180
 QY 181 QMORADISGYIPNGEWDLVGIPGKRSERYECCKEPYDPVTVTWMRRRTLYYGLNLIP 240
 DB 181 QMORADISGYIPNGEWDLVGIPGKRSERYECCKEPYDPVTVTWMRRRTLYYGLNLIP 240
 QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTVFMLVAEIMPATSDSVPLIAQYFAST 300
 DB 241 CVLISALALLVFLPADSGEKISLGITVLLSLTVFMLVAEIMPATSDSVPLIAQYFAST 300
 QY 301 MIIVGLSVVTVIVLQYHHDPDGGKMPKWTIRVILLNCAWFLRMKRPGEKVRPACQHK 360
 DB 301 MIIVGLSVVTVIVLQYHHDPDGGKMPKWTIRVILLNCAWFLRMKRPGEKVRPACQHK 360
 QY 361 QRCSLASVEMSAVAPPASNGNLLYIGRGLDGVHCVPPTDPSGVVCGMACSPHDEHL 420
 DB 361 QRCSLASVEMSAVAPPASNGNLLYIGRGLDGVHCVPPTDPSGVVCGMACSPHDEHL 420
 QY 421 LHGGOPPEGDPLAKILBEVRYIANRFRQDESEAVCSWKFAACVDRLCIMAFSVFTI 480
 DB 421 LHGGOPPEGDPLAKILBEVRYIANRFRQDESEAVCSWKFAACVDRLCIMAFSVFTI 480
 QY 481 ICTIGILMSAPNFVEAVSKDFA 502
 DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 2

G02259
 alpha 7 neuronal nicotinic acetylcholine receptor - human
 C:Species: Homo sapiens (man)
 C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 20-Aug-1999
 C:Accession: G02259
 R:Leonard, S.
 submitted to the EMBL Data Library, November 1995
 A:Reference number: H00936
 A:Accession: G02259
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-502 <LEO>
 A:Cross-references: EMBL:U40583; NID:g1125076; PIDN:AAA83561.1; PID:g1125077
 C:Superfamily: acetylcholine receptor

Query Match 99.7%; Score 2694; DB 2; Length 502;
 Best Local Similarity 99.6%; Pred. No. 1.7e-224;
 Matches 500; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAALASLLHVSLOGEFQRLKYLKYNPLERPVANDSQPLTVYFSLIL 60
 DB 1 MRCSPGGVWLAALASLLHVSLOGEFQRLKYLKYNPLERPVANDSQPLTVYFSLIL 60
 QY 61 QIMDVDEKNOVLTTNIWLQMSWDHYLQWNVSEYGVKTVRPDQGIWKPDIILLNSADE 120
 DB 61 QIMDVDEKNOVLTTNIWLQMSWDHYLQWNVSEYGVKTVRPDQGIWKPDIILLNSADE 120
 QY 121 RFDAFHTNVLVNSGHCQYLPPGIFKSSCYIDVRWFFPDVQCHCKLKFGSWYGGWSL 180
 DB 121 RFDAFHTNVLVNSGHCQYLPPGIFKSSCYIDVRWFFPDVQCHCKLKFGSWYGGWSL 180
 QY 181 QMORADISGYIPNGEWDLVGIPGKRSERYECCKEPYDPVTVTWMRRRTLYYGLNLIP 240
 DB 181 QMORADISGYIPNGEWDLVGIPGKRSERYECCKEPYDPVTVTWMRRRTLYYGLNLIP 240

QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTVFMLVAEIMPATSDSVPLIAQYFAST 300
 DB 241 CVLISALALLVFLPADSGEKISLGITVLLSLTVFMLVAEIMPATSDSVPLIAQYFAST 300
 QY 301 MIIVGLSVVTVIVLQYHHDPDGGKMPKWTIRVILLNCAWFLRMKRPGEKVRPACQHK 360
 DB 301 MIIVGLSVVTVIVLQYHHDPDGGKMPKWTIRVILLNCAWFLRMKRPGEKVRPACQHK 360
 QY 361 QRCSLASVEMSAVAPPASNGNLLYIGRGLDGVHCVPPTDPSGVVCGMACSPHDEHL 420
 DB 361 QRCSLASVEMSAVAPPASNGNLLYIGRGLDGVHCVPPTDPSGVVCGMACSPHDEHL 420
 QY 421 LHGGOPPEGDPLAKILBEVRYIANRFRQDESEAVCSWKFAACVDRLCIMAFSVFTI 480
 DB 421 LHGGOPPEGDPLAKILBEVRYIANRFRQDESEAVCSWKFAACVDRLCIMAFSVFTI 480
 QY 481 ICTIGILMSAPNFVEAVSKDFA 502
 DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 3
 A57175
 nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 20-Aug-1999
 C:Accession: A57175
 R:Ort-Urtreger, A.; Seldin, M.F.; Baldini, A.; Beaudet, A.L.
 Genomics 26, 399-402, 1995
 A:Title: Cloning and mapping of the mouse alpha7-neuronal nicotinic acetylcholine rec
 A:Reference number: A57175; MUID:95324936; PMID:7601470
 A:Accession: A57175
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-502 <ORR>
 A:Cross-references: GB:L37663; NID:g790853; PIDN:AAC42053.1; PID:g790854
 C:Superfamily: acetylcholine receptor
 C:Keywords: brain; glycoprotein; ion channel; neurotransmitter receptor; phosphoprote
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status pr
 F:231-254/Domain: transmembrane #status predicted <TR1>
 F:262-280/Domain: transmembrane #status predicted <TR2>
 F:296-317/Domain: transmembrane #status predicted <TR3>
 F:470-488/Domain: transmembrane #status predicted <TR4>
 F:46.90.133/Binding site: carbohydrate (Aen) (covalent) #status predicted
 F:365.413.427/Binding site: phosphate (Ser) (covalent) #status predicted
 F:415/Binding site: phosphate (Thr) (covalent) #status predicted
 F:442/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 94.3%; Score 2549; DB 2; Length 502;
 Best Local Similarity 94.0%; Pred. No. 5.5e-212;
 Matches 467; Conservative 18; Mismatches 12; Indels 0; Gaps 0;

QY 6 GGVWLAALASLLHVSLOGEFQRLKYLKYNPLERPVANDSQPLTVYFSLILQIMDV 65
 DB 6 GGVWLAALASLLHVSLOGEFQRLKYLKYNPLERPVANDSQPLTVYFSLILQIMDV 65
 QY 66 DEKNQVLTTNIWLQMSWDHYLQWNVSEYGVKTVRPDQGIWKPDIILLNSADERFAT 125
 DB 66 DEKNQVLTTNIWLQMSWDHYLQWNVSEYGVKTVRPDQGIWKPDIILLNSADERFAT 125
 QY 126 FHTNVLVNSGHCQYLPPGIFKSSCYIDVRWFFPDVQCHCKLKFGSWYGGWSLQMOEA 185
 DB 126 FHTNVLVNSGHCQYLPPGIFKSSCYIDVRWFFPDVQCHCKLKFGSWYGGWSLQMOEA 185
 QY 186 DISGYIPNGEWDLVGIPGKRSERYECCKEPYDPVTVTWMRRRTLYYGLNLIPCVLIS 245
 DB 186 DISGYIPNGEWDLVGIPGKRSERYECCKEPYDPVTVTWMRRRTLYYGLNLIPCVLIS 245
 QY 246 ALALLVFLPADSGEKISLGITVLLSLTVFMLVAEIMPATSDSVPLIAQYFASTMIIVG 305
 DB 246 ALALLVFLPADSGEKISLGITVLLSLTVFMLVAEIMPATSDSVPLIAQYFASTMIIVG 305

QY 306 LSVVTVTVLQVHHDDPGGKMPKWTTRVILLNWCAMFLRMKRPGEKVPACQHKQRCS 365
DB 306 LSVVTVTVLQVHHDDPGGKMPKWTTRVILLNWCAMFLRMKRPGEKVPACQHKQRCS 365
QY 366 LASVEMSAVAPPASNGNLLYIGFRGLDGVCHVCTPTDPSGVVCGMACSPTHDEHLHGQ 425
DB 366 LASVELSAGAPPTSNGNLLYIGFRGLEGMHCAPTDPDSGVVCGRLACSPTHDEHLMHGTH 425
QY 426 PPEGDDPLAKILEEVRYIANRFRQDESEAVCSSEKFAACVVDRLCLMAFVSFTIICITG 485
DB 426 PSDGDDPLAKILEEVRYIANRFRQDESEVICSEKFAACVVDRLCLMAFVSFTIICITG 485
QY 486 ILMSAPNFVEAVSKOFA 502
DB 486 ILMSAPNFVEAVSKOFA 502

RESULT 4
T01378
nicotinic receptor alpha 7 chain - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 21-Jul-2000
C:Accession: T01378
R;Seguella, P.; Madiche, J.; Dineley-Miller, K.; Dani, J.A.; Patrick, J.W.
J. Neurosci. 13, 596-604, 1993
A:Title: Molecular cloning, functional properties, and distribution of rat brain alpha 7
A:Reference number: Z14310; MUID:93147931; PMID:7678857
A:Accession: T01378
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-502 <SEG>
A:Cross-references: EMBL:S53987; NID:g264770; PIDN:AA25224.2; PID:g5705903
A:Experimental source: brain
A:Superfamily: acetylcholine receptor

Query Match 93.8%; Score 2535; DB 2; Length 502;
Best Local Similarity 93.6%; Pred. No. 9e-211;
Matches 465; Conservative 18; Mismatches 14; Indels 0; Gaps 0;

QY 6 GGVWLAALAAALLVSLQGEFORKLYKELVKNYNPLRPVANDSQPLTVYFSLSLQIMDV 65
DB 6 GGVWLAALAAALLVSLQGEFORKLYKELVKNYNPLRPVANDSQPLTVYFSLSLQIMDV 65
QY 66 DERNOVLTNIWLQMSWTDHYLQNVSEYFGVKTVPDQGIWKPDILLNSADERFDT 125
DB 66 DERNOVLTNIWLQMSWTDHYLQNVSEYFGVKNVFPDQGIWKPDILLNSADERFDT 125
QY 126 FHTNVLNNSGHCQYLPFGIKSSCYIDVRFPDVOHCKLKFGSWSYGWSLDLQMOEA 185
DB 126 FHTNVLNNSGHCQYLPFGIKSSCYIDVRFPDVOHCKLKFGSWSYGWSLDLQMOEA 185
QY 186 DISYIPIGWDVLGIPGKSEREYECCKEPYDVTFVTWRRRLTYGLNLLIPCVLIS 245
DB 186 DISYIPIGWDVLGIPGKNEKEEYECCKEPYDVTFVTWRRRLTYGLNLLIPCVLIS 245
QY 246 ALALLVFLPADSGEKISLGIITVLLSTVFMLLVAEIMPATSDSVPLIAQYFASFTMIIG 305
DB 246 ALALLVFLPADSGEKISLGIITVLLSTVFMLLVAEIMPATSDSVPLIAQYFASFTMIIG 305
QY 306 LSVVTVTVLQVHHDDPGGKMPKWTTRVILLNWCAMFLRMKRPGEKVPACQHKQRCS 365
DB 306 LSVVTVTVLQVHHDDPGGKMPKWTTRVILLNWCAMFLRMKRPGEKVPACQHKQRCS 365
QY 366 LASVEMSAVAPPASNGNLLYIGFRGLDGVCHVCTPTDPSGVVCGMACSPTHDEHLHGQ 425
DB 366 LASVELSAGAPPTSNGNLLYIGFRGLEGMHCAPTDPDSGVVCGRLACSPTHDEHLMHGTH 425
QY 426 PPEGDDPLAKILEEVRYIANRFRQDESEAVCSSEKFAACVVDRLCLMAFVSFTIICITG 485
DB 426 PSDGDDPLAKILEEVRYIANRFRQDESEVICSEKFAACVVDRLCLMAFVSFTIICITG 485
QY 486 ILMSAPNFVEAVSKOFA 502
DB 486 ILMSAPNFVEAVSKOFA 502

DB 486 ILMSAPNFVEAVSKOFA 502

RESULT 5
JN0113
nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - chicken
N:Alternate names: alpha-bungarotoxin-binding protein alpha chain
C:Species: Gallus gallus (Chicken)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 20-Aug-1999
C:Accession: JN0113; JH0172; S28018; B25738; S26566
R;Coururier, S.; Bertrand, D.; Matter, J.M.; Hernandez, M.C.; Millar, N.
Neuron 5, 847-856, 1990
A:Title: A neuronal nicotinic acetylcholine receptor subunit (alpha 7) is developmenta
A:Reference number: JN0113; MUID:91097796; PMID:1702646
A:Accession: JN0113
A:Molecule type: DNA
A:Residues: 1-502 <CON>
A:Cross-references: GB:X68586; NID:g287756; PIDN:CAA48576.1; PID:g287757
A:Experimental source: white leghorn; brain
R;Schoepfer, R.; Conroy, W.G.; Whiting, P.; Gore, M.; Lindstrom, J.
Neuron 5, 35-48, 1990
A:Title: Brain alpha-bungarotoxin binding protein cDNAs and MAb reveal subtypes of th
A:Reference number: JH0172; MUID:90315158; PMID:2369519
A:Accession: JH0172
A:Molecule type: mRNA
A:Residues: 1-502 <SCH>
A:Cross-references: EMBL:X52295; NID:g63077; PIDN:CAA36543.1; PID:g63078
A:Experimental source: brain
R;Watter-Sadzinski, L.; Hernandez, M.C.; Rostocil, T.; Ballivet, M.; Matter, J.M.
EMBO J. 11, 4529-4538, 1992
A:Title: Neuronal specificity of the alpha7 nicotinic acetylcholine receptor promoter
A:Reference number: S28018; MUID:93049204; PMID:1425587
A:Accession: S28018
A:Molecule type: DNA
A:Residues: 1-18 <MAS>
A:Cross-references: EMBL:X68246; GB:S49751; NID:g65319; PIDN:CAA48317.1; PID:g65320
A:Experimental source: white leghorn; erythrocyte
R;Conti-Tronconi, B.M.; Dunn, S.M.J.; Barnard, E.A.; Dolly, J.O.; Lai, F.A.; Ray, N.; J
Proc. Natl. Acad. Sci. U.S.A. 82, 5208-5212, 1985
A:Title: Brain and muscle nicotinic acetylcholine receptors are different but homologou
A:Reference number: A94055; MUID:85270494; PMID:3860855
A:Accession: B25738
A:Molecule type: protein
A:Residues: 24-25, 27, 28-41, X', 43-45, X', 47 <CON>
C:Comment: This acetylcholine receptor is blocked by alpha-bungarotoxin and is localiz
C:Genetics:
A:Introns: 19/1; 65/3; 80/3; 117/2; 144/1; 200/1; 265/1; 294/1; 330/3
A:Superfamily: acetylcholine receptor
C:Keywords: brain; glycoprotein; ion channel; neurotransmitter receptor; phosphoprotei
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status pre
F;231-254/Domain: transmembrane #status predicted <TR1>
F;262-280/Domain: transmembrane #status predicted <TR2>
F;296-317/Domain: transmembrane #status predicted <TR3>
F;470-488/Domain: transmembrane #status predicted <TR4>
F;46,90,133/Binding site: carboxydrate (Asn) (covalent) #status predicted
F;365,367,413,427,465/Binding site: phosphate (Ser) (covalent) #status predicted
F;415/Binding site: phosphate (Thr) (covalent) #status predicted
F;442/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 90.0%; Score 2433; DB 2; Length 502;
Best Local Similarity 90.9%; Pred. No. 5.7e-202;
Matches 450; Conservative 18; Mismatches 27; Indels 0; Gaps 0;

QY 8 VTLAAALAAALLVSLQGEFORKLYKELVKNYNPLRPVANDSQPLTVYFSLSLQIMDVDE 67
DB 8 LMLAAAGLVRESLQGEFORKLYKELVKNYNPLRPVANDSQPLTVYFSLSLQIMDVDE 67
QY 68 KNOVLTTNIWLQMSWTDHYLQNVSEYFGVKTVPDQGIWKPDILLNSADERFDTFH 127
DB 68 KNOVLTTNIWLQMSWTDHYLQNVSEYFGVKNVFPDQGIWKPDILLNSADERFDTFH 127
QY 128 TTNVLNNSGHCQYLPFGIKSSCYIDVRFPDVOHCKLKFGSWSYGWSLDLQMOEADI 187
DB 128 TTNVLNNSGHCQYLPFGIKSSCYIDVRFPDVOHCKLKFGSWSYGWSLDLQMOEADI 187

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Db      128  TNVLVNSGHCQYLPGLFKSSCYIDVAFDFDQKCNLKFSGWTYGGWSDLLQMQEADI 187
QY      188  SGYIPNGEWDLVIGPKSERFYECCKEPYDPDVTFTVMRRRTLYYGLNLIPCVLISAL 247
Db      188  SGYIPNGEWDLVIGPKSERFYECCKEPYDPDVTFTVMRRRTLYYGLNLIPCVLISAL 247
QY      248  ALLVFLPADSGEKISLGLTLLSLTVMFLVAETMPATSDSVPLIAQYFASFTMLIVGLS 307
Db      248  ALLVFLPADSGEKISLGLTLLSLTVMFLVAETMPATSDSVPLIAQYFASFTMLIVGLS 307
QY      308  VVVTVIVLQYHHDDPGGKMPKTRVILLNWCAMFLRMKRPGEKVRPACQHKQRCSLA 367
Db      308  VVVTVIVLQYHHDDPGGKMPKTRVILLNWCAMFLRMKRPGEKVRPACQHKQRCSLS 367
QY      368  SVEMSAVAPPASNGNLIIYIGRGLDGVHCVPTDPSGVVCGRMACSPHDEHLLGGQPP 427
Db      368  SVEMNTVSGQQCSNGNLIIYIGRGLDGVHCVPTDPSGVVCGRMACSPHDEHLLGGQPP 427
QY      428  EGDPLAKILEVRVIANFRQDESEAVCSWKFAACVVDRLCLMAFSVFTIICIGIL 487
Db      428  EGDPLAKILEVRVIANFRQDESEAVCSWKFAACVVDRLCLMAFSVFTIICIGIL 487
QY      488  MSAPNFVEAVSKDFA 502
Db      488  MSAPNFVEAVSKDFA 502

RESULT 6
JH0173
A:Title: Brain alpha-bungarotoxin binding protein cDNAs and MABs reveal subtypes of this
A:Species: Gallus gallus (chicken)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 20-Aug-1999
C:Accession: JH0173
R:Schaeffer, R.; Conroy, W.G.; Whiting, P.; Gore, M.; Lindstrom, J.
Neuron 5, 35-48, 1990
A:Note: This sequence is similar to acetylcholine receptor alpha chains
A:Reference number: JH0172; MUID:90315158; PMID:2369519
A:Accession: JH0173
A:Molecule type: mRNA
A:Cross-references: GB:X52296; NID:G63081; PIDN:CAA35544.1; PID:G63082
A:Experimental source: brain
C:Comment: Alpha-bungarotoxin binding proteins are localized to extrasynaptic pseudodend
C:Superfamily: acetylcholine receptor
C:Keywords: glycoprotein; transmembrane protein
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-510/Product: alpha-bungarotoxin binding protein alpha-2 chain #status predicted <AB
F:239-262/Domain: transmembrane #status predicted <TM1>
F:270-288/Domain: transmembrane #status predicted <TM2>
F:304-323/Domain: transmembrane #status predicted <TM3>
F:479-496/Domain: transmembrane #status predicted <TM4>
F:54/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      67.4%; Score 1820.5; DB 2; Length 511;
Best Local Similarity 69.0%; Pred. No. 4.4e-149;
Matches 343; Conservative 56; Mismatches 93; Indels 5; Gaps 4;

QY      8  VWLAAASLLHVSQGEFQKLYKELVKNYNPLERPVANDSQPLTYVFSLSLLOIMDVDE 67
Db      16  LWASFLSFSPKVSQGESQRRLYDLRNLYRNLERPVANDSQPIVVELQSLQIIDVDE 75
QY      68  KNOVLTTNIWLQSWTDHYLQWNVSEYPGVKTVRPDQGIWKPDILLNYSADRFDATFH 127
Db      76  KNOVLITNAWLQYWDIYLSWQYEPGVQNLRFPSDQIWKPDILLNYSADRFDATFH 135
QY      128  TNVLVNSGHCQYLPGLFKSSCYIDVAFDFDQKCNLKFSGWSDLLQMQEADI 187
Db      136  TNVLVNSGHCQYLPGLFKSSCYIDVAFDFDQKCNLKFSGWSDLLQMQEADI 195
QY      188  SGYIPNGEWDLVIGPKSERFYECCKEPYDPDVTFTVMRRRTLYYGLNLIPCVLISAL 247

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Db      196  SNYISNGEWDLVGPVKRKNELYECCKEYDPDVTFTVMRRRTLYYGLNLIPCVLISGL 255
QY      248  ALLVFLPADSGEKISLGLTLLSLTVMFLVAETMPATSDSVPLIAQYFASFTMLIVGLS 307
Db      256  ALLVFLPADSGEKISLGLTLLSLTVMFLVAETMPATSDSVPLIAQYFASFTMLIVGLS 315
QY      308  VVVTVIVLQYHHDDPGGKMPKTRVILLNWCAMFLRMKRPGEKVRPACQHK--QRRC 364
Db      316  VVVTVIVLQYHHDDPGGKMPKTRVILLNWCAMFLRMKRPGEKVRPACQHK--QRRC 374
QY      365  SLASVEMSAVAPPASNGNLIIYIGRGLDGVHCVPTDPSGVVCGRMACSPHDEHLLGG 424
Db      375  SLKNTNVLVSGHOPSGNGNMIY-SYHTMENPCCQNNDLGSKSGKITCPLSEDEHVQKK 433
QY      425  QPPSGDPLAKILEVRVIANFRQDESEAVCSWKFAACVVDRLCLMAFSVFTIICIT 484
Db      434  ALMDTIPVIVKILEVQFIAMFRKQDEGEICSEWKFAAAVVDRLCLVAFTLFAITCTF 493
QY      485  GILMSAPNFVEAVSKDF 501
Db      494  TILMSAPNFIEAVSKDF 510

RESULT 7
S68588
A:Title: Nicotinic acetylcholine receptors in the nematode Caenorhabditis elegans.
A:Species: Caenorhabditis elegans
C:Date: 06-Dec-1996 #sequence_revision 07-Feb-1997 #text_change 20-Aug-1999
C:Accession: S68588; S57496
R:Ballivet, M.; Alliod, C.; Bertrand, S.; Bertrand, D.
J. Mol. Biol. 258, 261-269, 1996
A:Title: Nicotinic acetylcholine receptors in the nematode Caenorhabditis elegans.
A:Reference number: S68587; MUID:96196478; PMID:8627624
A:Accession: S68588
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-498 <BAL>
A:Cross-references: EMBL:X83887; NID:G872087; PIDN:CAA58764.1; PID:G872088
C:Superfamily: acetylcholine receptor
C:Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membr
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-498/Product: nicotinic acetylcholine receptor alpha-1 chain #status predicted <M

Query Match      41.0%; Score 1108.5; DB 2; Length 498;
Best Local Similarity 44.6%; Pred. No. 1.3e-87;
Matches 226; Conservative 77; Mismatches 167; Indels 37; Gaps 7;

QY      10  LALAASLLHVSQGEFQKLYKELVKNYNPLERPVANDSQPLTYVFSLSLLOIMDVDEK 68
Db      6  LLISCAILAAAPTGLSLOERLYEDLRNLYRNLERPVANHSPEVTVHLKVALQOIIDVDEK 65
QY      69  NOVLTTNIWLQSWTDHYLQWNVSEYPGVKTVRPDQGIWKPDILLNYSADRFDATFH 128
Db      66  NOVTVNAWLDYTNWYDNLVWDKAYGNITDVRFFAGKIWKPDVLLNYSVDINFDSTYQT 125
QY      129  NVLVNSGHCQYLPGLFKSSCYIDVAFDFDQKCNLKFSGWSDLLQMQEA--D 186
Db      126  NMIVYSTGLVHWVPPGIFKISCKIDIQWPPFDEQKCFKFGSWTYDGYKLIQATGGPD 185
QY      187  ISGYIPNGEWDLVIGPKSERFYECCKEPYDPDVTFTVMRRRTLYYGLNLIPCVLISA 246
Db      186  ISEYISNGEWALPLTIVTERNEKFPYDCCPEYPDVHFYLMRRRTLYYGNLIMPICITL 245
QY      247  LALLVFLPADSGEKISLGLTLLSLTVMFLVAETMPATSDSVPLIAQYFASFTMLIVGL 306
Db      246  WTLGLFTLPDAGEKITQITVLLSICFSLVSEMSPTSEAVPLIGIFFCCMVVTA 305
QY      307  VVVTVIVLQYHHDDPGGKMPKTRVILLNWCAMFLRMKRPGEKVRPACQHKQRCSL 366
Db      306  STVFTVYVNLNHYRTPETHDMGPTNRNLLLYIPWILRMKRPG-----HNLTYASL 356
QY      367  ASVEMSAVAPPASNGNLIIYIGRGLDGVHCVPTDPS-----GVVCGMAC 412

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Db 357 PSL-----FSTKPNRHSRLIRNIK--DNEHSLGRANSFADACRLNQVIMTQSVNSGLTSL 410
QY 413 SPTHDEHLLHGGQPPEGDPD-----LAKILEEVRVYIANFRFCODESAVCSWKFAACV 467
Db 411 GSTPSTWISSNGTITVDSQATLLILHRIYHEUKIVTKRMIEGDKKEQACNNKFAAMV 470
QY 468 DRLCIMAFSVFTICTIGILMSAPNFV 494
Db 471 DRCLXYVFTIIVSTIGIFWASPYLV 497

RESULT 8
T19622
hypothetical protein C31H5.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T19622
R:Kershaw, J.
submitted to the EMBL Data Library, April 1997
A:Reference number: Z19153
A:Accession: T19622
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-560 <WIL>
A:Cross-references: EMBL:Z93778; PIDN: CAB07843.1; GSPDB: GN00019; CESP: C31H5.3
A:Experimental source: clone C31H5
C:Genetics:
A:Gene: CESP: C31H5.3
A:Map position: 1
A:Introns: 24/1; 70/3; 139/2; 270/1; 299/1; 336/3; 372/2; 456/3
C:Superfamily: acetylcholine receptor

Query Match 40.5%; Score 1093.5; DB 2; Length 560;
Best Local Similarity 40.8%; Pred. No. 2.9e-86;
Matches 227; Conservative 93; Mismatches 156; Indels 81; Gaps 9;

QY 10 LALAASLI-----HVSLOGEFORKLYKEIVKNYNPLERPANDSOPLTIVFSLSLQI 62
Db 8 LVLSVSLIWEKCKSVIWTGDHERRLYAKLAENYKILARPVRNESEAVVLLGMDYQOI 67
QY 63 MDVDEKQVLTNTLWQSWTDHLYQWNVSEYPGVKTVRFPDQGIWKQIDILLYNSADERF 122
Db 68 LDIDEXQIMNSNWLKMSWDHLYTWPDSFNGIKVEKRLPINNIWKPDVLLYNSVDQOF 127
QY 123 DATHTNVLNNSGHCOYLPPIKSCYIDVRWPPDVQCKLKFSGWSYGGNSLDQM 182
Db 128 DSTWPNVAVLYTGNVTPALIRSSCAIDIAFPPTQCTWKFSGWTSYGFDTDLIN 187
QY 183 QEADISGYIPNGEWDLVGIPGKRSERFYECCKEPYPDVFTVMRRRTLYYGLMLIPCV 242
Db 188 TTISPATYKPNGEWELLGLTSQSRISFFYECCPEPYDVTFTVIRRTLYYGFNLLPCM 247
QY 243 LISALALVFLPADSGEKISIGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFASPMI 302
Db 248 LISSALLSFTLPADCGEKLNGVTFMSLCVFMVAEAMPQTSDAFLPIQIYFSCIMF 307
QY 303 IVGLSVVTVTVIYQVHHDDPGGK-MPKWTRVILLNWCAMFLMRKPGEDKVRPACQ-- 359
Db 308 QVGSVAIVATVIANFHRHSPEQYKPMKFKLLTLLGLMFTLLGMRPDLVLSVHGAYHA 367
QY 360 ----KQRCISLASVEMSAVAPPASNGNLLYIGFGLD----- 393
Db 368 SONKKKQRYLVEVERHILTRP-----NGN-----GHSADVAKVHLDLSTGNPHSDAKKSPS 420
QY 394 -----GVICVTP-----DSGV---VGRMACSPTDHEHLLHGGQPEGDP----- 431
Db 421 PKRTSASINGMTGLPTQMGALDSINKYCTKVTPLNGSATINHKSSQPININN 480
QY 432 -----DLAKILEEVRVYIANFRFCODESAVCSWKFAACVDRLCIMAF 475
Db 481 NIYKCANNOKTOFEDRPHPHILNELRVISARVKEEMHALQADWVFASVVDVRCFLAF 540
QY 476 SVFTIICTIGILMSAPN 492

Db 541 SAFLFMCTAIISYNAPH 557

RESULT 9
T25671
hypothetical protein D2092.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T25671
R:Gattung, S.; Maggi, L.
submitted to the EMBL Data Library, February 1997
A:Description: The sequence of C. elegans cosmid D2092.
A:Reference number: Z20067
A:Accession: T25671
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-461 <GAT>
A:Cross-references: EMBL:U88167; PIDN: AAB42223.1; GSPDB: GN00019; CESP: D2092.3
A:Experimental source: strain Bristol N2; clone D2092
C:Genetics:
A:Gene: CESP: D2092.3
A:Map position: 1
A:Introns: 36/1; 80/3; 119/2; 191/1; 243/1; 274/1; 303/1; 382/2
C:Superfamily: acetylcholine receptor

Query Match 37.0%; Score 999; DB 2; Length 461;
Best Local Similarity 39.8%; Pred. No. 3.2e-78;
Matches 197; Conservative 96; Mismatches 146; Indels 56; Gaps 8;

QY 12 LAASLIHVSIL-QGEF-ORKLYKEIVKNYNPLERPANDSOPLTIVFSLSLQIMDVDEKN 69
Db 10 LSLVLIHNSLDCGSAETKLTLLKGNPLERPVQNSQPLEVKIKLFLQQLILDVDEKN 69
QY 70 QVLTNTLWQSWTDHLYQWNVSEYPGVKTVRFP--DQIWKPDILLYNSADERFDATEH 127
Db 70 QIVSVNWLSTVTFDHLQWEPKKGIGIQDIRFPSSDHIWKPDLVLYNSAAEDFSTFK 129
QY 128 TNVLNNSSGHCQYLPPIKSCYIDVRWPPDVQCKLKFSGWSYGGNSLDQM----- 182
Db 130 SNLLTYHTGTVMVPPGVLFVQCQDVTWFPDDQVCEMKFGSWTFHGYAIDLQIDDDTN 189
QY 183 --QEADISGYIPNGEWDLVGIPGKRSERFYECCKEPYPDVFTVMRRRTLYYGLMLIP 240
Db 190 GTQSMDSLTVLVNGEWOVISTNAKRVSYKCCPEPYTVNYIHRRTLYYGFNLLIP 249
QY 241 CVLISALALVFLPADSGEKISIGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFASPMI 300
Db 250 SLLISLMAILGFMPPDRGEKILTEVLLIAIVFLSNVSEMTPTSEAVPLIGVFFSCC 309
QY 301 MIIVGLSVVTVTVIYQVHHDDPGGKMPKWKTRVILLNWCAMFLMRKPGEDKVRPACQHK 360
Db 310 MLVVSASVFTVIVLNLHFRSADSHEMNPLVRRVLLLEFLPWLFLMSPRGYKFKV----- 363
QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGFGLDGVHCVPTPDSGVVCGRMACSPTHDEH 419
Db 364 ----ANV-----IDSTKMPKPKPKPLDCLNPSNHAGYEAQ 395
QY 420 LLHGQPEGDPDLAKILLEEVRVYIANFRFCODESAVCSWKFAACVVDRLCLMAFSVFT 479
Db 396 ILL-----LHVSHTELRRVAVFYNKEHDERIQTDRFAAMVVDRACLLLFTTVEI 445
QY 480 ICTIGILMSAPNFV 494
Db 446 VISILAINMSAPHII 460

RESULT 10
S12359
nicotinic acetylcholine receptor alpha-L1 chain precursor - desert locust
C:Species: Schistocerca gregaria (desert locust)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
C:Accession: S12359

R;Marshall, J.; Buckingham, S.D.; Shingai, R.; Lunt, G.G.; Goosey, M.W.; Darlison, M.G.; EMBO J. 9, 4391-4398, 1990
 A;Title: Sequence and functional expression of a single alpha subunit of an insect nicotinic A;Reference number: S12359; MUID:91092263; PMID:1702381
 A;Accession: S12359
 A;Molecule type: mRNA
 A;Residues: 1-557 <MAR>
 A;Cross-references: EMBL:X55439; NID:g10133; PIDN:CAA39081.1; PID:g10134
 C;Superfamily: acetylcholine receptor
 C;Keywords: glycoprotein; ion channel; neurotransmitter receptor; transmembrane protein
 F;1-23/Domain: signal sequence #status predicted <SIG>
 F;24-557/Product: nicotinic acetylcholine receptor alpha-L1 chain #status predicted <MAT>
 F;245-266/Domain: transmembrane #status predicted <TM1>
 F;274-295/Domain: transmembrane #status predicted <TM2>
 F;308-329/Domain: transmembrane #status predicted <TM3>
 F;501-523/Domain: transmembrane #status predicted <TM4>
 F;47,235/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 35.1%; Score 949; DB 2; Length 557;
 Best Local Similarity 37.1%; Pred. No. 8.5e-74;
 Matches 201; Conservative 93; Mismatches 176; Indels 72; Gaps 6;

QY 5 PGGVWLAASLLHVSQGEFQKLYKELVKNVPLRPVANDSQPLTVFSLSLQIMD 64
 DB 6 PMLLLLLLLHHPAAAPDAKRLYDLSNRLIRVSNNTDTVLKGLGLSLQID 65
 QY 65 VDEKNQVLTNIWLSQSWTDHYLQWNVSEYPGVKTVPDQGIWKPDIILYNSADREFDA 124
 DB 66 LNLKQILITNVWLEHWDHKEPDAEYGGVTELYVSEHILWLPDIVLNNADGEYVV 125
 QY 125 THTNVLVNSGCHQYLPFGIFKSSCYIDVRWPPFVQVCKLKFGSWGSLDQ--- 181
 DB 126 TMTKAVLHHTGKVVWTPPAIFKSSCEIDVRYPFQQTCFMKFGSWTYDGDQIDLKHN 185
 QY 182 -----MQEADISYIPNGEWDLYGIPKRSERYECCKEPYDPVTVTMRRTLY 233
 DB 186 QYDDNKVKVIGIDIREYPSVEWDILGPAERHEKYPCCAEYPDIFNITLRRKTLFY 245
 QY 234 GLNLLPCVLISALALLVFLPADSGEKISLGTIVLLSLTVFLLVAEIMPATSDSVPLI 293
 DB 246 TVNLIIVPCVIGISLVFLPADSGEKIALCISILLQTMFFLLSEIIPSTSLALPL 305
 QY 294 AQVFASTMIIVGSLVTVLYQYHHDPDGGKPKWTRVILLNWCWFLMRKRPGE--- 350
 DB 306 GKYLFTWLVGLSVTTIMLVNHYVKPSTHMAFWKVFTRRLPKLLMRVPEQLLA 365
 QY 351 DKVRPACQKQRCRCSLAVMSAVAPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRM 410
 DB 366 DLASKRLLRHNSKLSAAAAAASSS-----AASSPDS--LRHHH 408
 QY 411 ACSPTHDEHL-LHGGOPPEG----- 429
 DB 409 LHQHQHHLQLHLQRFPGCGNGLHSATNRFSGSAGAFGLPSVVGDLGSLSDVATRK 468
 QY 430 DPDLAKILEVRVIANFRQDSEAVCSWKAACVDRCLMARSVFTIITIGILMS 489
 DB 469 PFELEKAHNVLFIQNHQDQDFDARDQWGFVAMVLDRLFLFIATISVGTFAILCE 528
 QY 490 AP 491
 DB 529 AP 530

RESULT 11
 A40110
 nicotinic acetylcholine receptor alpha-2 chain precursor - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 20-Mar-1992 #sequence_revision 10-Apr-1992 #text_change 20-Aug-1999
 C;Accession: A40110
 R;Wada, K.; Ballivet, M.; Boulter, J.; Connolly, J.; Wada, E.; Deneris, E.S.; Swanson, L. Science 240, 330-334, 1988
 A;Title: Functional expression of a new pharmacological subtype of brain nicotinic acetylcholine receptor
 A;Reference number: A40110; MUID:88178113; PMID:2832952

A;Accession: A40110
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-511 <WAD>
 A;Cross-references: GB:M20297; NID:g202672; PIDN:AAA40664.1; PID:g202674
 A;Note: the authors translated the codon TCG for residue 494 as Cys
 C;Superfamily: acetylcholine receptor
 C;Keywords: neurotransmitter receptor

Query Match 35.0%; Score 946.5; DB 2; Length 511;
 Best Local Similarity 39.1%; Pred. No. 1.3e-73;
 Matches 202; Conservative 83; Mismatches 178; Indels 53; Gaps 9;

QY 8 VW-LALAASLLHVSQGEFQKLYKELVKNVPLRPVANDSQPLTVFSLSLQIMDV 65
 DB 16 IMCLLIVPAVLTVQSSHTHAEDRLFKHLFGGYNRWARPVPNTSDVVVRFGLSIAQLIDV 75
 QY 66 DEKNQVLTNIWLSQSWTDHYLQWNVSEYPGVKTVPDQGIWKPDIILYNSADREFDA 125
 DB 76 DEKNQVLTNIWLSQSWTDHYLQWNVSEYPGVKTVPDQGIWKPDIILYNSADREFDA 135
 QY 126 FHTNVLVNSGCHQYLPFGIFKSSCYIDVRWPPFVQVCKLKFGSWGSLDQIMQ 184
 DB 136 HMTKAHLFTGTWVWPPPAIYKSSCSIDVTFEFDQCNCKMKFGSWTYDKAKIDLEQMER 195
 QY 185 -ADISGYIPNGEWDLYGIPKRSERYECCKEPYDPVTVTMRRTLYYGNLLIPCVL 243
 DB 196 TVDLKDYWESGEWAIINATGTYNSKKYDCAIYDPVTVYFVIRRLPLFTYINLIIPCLL 255
 QY 244 ISALLVFLPADSGEKISLGTIVLLSLTVFLLVAEIMPATSDSVPLIAQVFASTMI 303
 DB 256 ISCLTVLFLPADSGEKITLCISVLLSLTVFLLIETIPSTSLVPIGLYLLFTMIF 315
 QY 304 VGLSVTVTVLYQYHHDPDGGKPKWTRVILLNWCWFLMRKRP-----GEDKVRA 356
 DB 316 VTLISVITVFLVNVHRSSTHNMNWRVALLGRVPRWLMNRRPLPMLHSGSPDLKLS 375
 QY 357 COHKQRCRCSLAVMSAVAPPASNGNLLYIGRGLDGVHCVPTPDS--GVVCGRMACSP 414
 DB 376 PSYHLEITNMDAGERETEETEBEEDENICV-----CAGLPDSSMGVLVG----- 420
 QY 415 THDEHLHGG-----QPPG-----DPDLAKILEEVRYIANRFRQDSEAVCS 458
 DB 421 -----HGGLHLMAREPETKTPSOASEILLSPQIKALEGVHYIADRLSRSDADSVKE 473
 QY 459 EMKFAACVVDRLCLMAFVFTIITIGILMSAPNFV 494
 DB 474 DKWYAMVVDRLFLFIIVSFLTIGLFL--PPFL 507

RESULT 12

T19862

hypothetical protein C40C9.2 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C;Accession: T19862

R;Hembry, C.

submitted to the EMBL Data Library, March 1996

A;Reference number: Z19188

A;Accession: T19862

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-542 <WIL>

A;Cross-references: EMBL:270266; PIDN:CAA94206.1; GSPDB:GN00028; CESP:C40C9.2

A;Experimental source: clone C40C9

C;Genetics:

A;Gene: CESP:C40C9.2

A;Map position: X

A;Introns: 11/3; 69/3; 123/2; 173/3; 216/1; 248/1; 279/1; 314/1; 350/3; 430/1; 464/1;

C;Superfamily: acetylcholine receptor

Query Match 35.0%; Score 945; DB 2; Length 542;

Best Local Similarity 37.7%; Pred. No. 1.8e-73;


```
Matches 207; Conservative 93; Mismatches 165; Indels 84; Gaps 15;
QY 11 ALAASLLHV-----SLQGFQRLKYLKELVQNNPRLRPVANDSOPLTVYFSLSLQIMDV 65
Db 12 ALHCVLHLLTEVHSSADEY--RLADLRHNDPYRPPVANASEPLWVSKYLOQILDV 69
QY 66 DEKNQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVPFPD--GOIKWPKDILLVNSADERED 123
Db 70 DEKNQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVPFPD--GOIKWPKDILLVNSADERED 129
QY 124 ATFTHTNLVNSGHCQYLPPIGFKSSCYIDVRFPDQVCHCKLKFGSWYGGWSLDLQM-- 182
Db 130 STVPNVVSVYTGDLVQVPPGILKLSCKIDITVFPDDQICHLKFGSWYSGNFIDLRIN 189
QY 183 -----QADISGIYPNGEWDLVGIPGKRSERFECCKEYKPYDVTFTVTRRETLAY 233
Db 190 GPEGKNIISDEGIDVQVYVQNGEWNLLAVPARHETNIFD--EQYPISLFFYLIITORTLYY 247
QY 234 GLNLLIPCVLISALALLVFLPADSGEKISLGTITVLLSLTVFMILVAEIMPATSDSVPLI 293
Db 248 GLNLLIPSPFLISLMTVLGFTLPDAGEKITLEITILLSVCFILSMVADMTPTTSEAVPLI 307
QY 294 -----AOYFASMTIIVGLSVVTVIVLQVHHHDPDGGKMPKWTIVILLNWCWAFIRMKR 347
Db 308 GLIIFSGAFSCCMVLVSASVFTVLVNLHNRKPEHETHEMSPFLREILLITWLPWLLIMRR 367
QY 348 PGEDKVRPACQKQRCRCLASVEMSAVAPPASNGNLLIYIG--FRGLDGVHCVPTPDG-- 404
Db 368 PG--KTIFNCTHLKAEAKKAGSGI-----KNG-----VGPKPTDSVH-----PSEGLS 412
QY 405 -----VVGCR--MACSPTHDEHLHGG-----OPPEGDP----- 431
Db 413 LMKNIKLGROQTIDFEYFHVQHNLMPVAPSEMTPTVTSKYMAESYVEDVWVTELNKY 472
QY 432 -----DLAKILBEVRYANFRQDESEAVCEWKFACVVDRLCLMAFVTTICTIGILMSAPNF 493
Db 473 MQKACLELNKISSQTRAMKMEDEDEQAANDKFAAMVVDRCCLITFSVFIVWSTCG 532
QY 486 ILMSAPNFV 494
Db 533 IMFSSPHLI 541

RESULT 13
S14703
nicotinic acetylcholine receptor beta-2 chain - goldfish (fragment)
C;Species: Carassius auratus (goldfish)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug-1999
C;Accession: S14703
R;Hieber, V.; Bouchey, J.; Agranoff, B.W.; Goldman, D.
Nucleic Acids Res. 18, 5307, 1990
A;Title: Nucleotide and deduced amino acid sequence of the goldfish neural nicotinic acetylcholine receptor
A;Reference number: S14703; MUID:90384858; PMID:2402468
A;Accession: S14703
A;Molecule type: mRNA
A;Residues: 1-459 <HTE>
A;Cross-references: EMBL:X54052; NID:G62576; PIDN:CAA37986.1; PID:g833601
C;Superfamily: acetylcholine receptor
C;Keywords: Glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane;

Query Match 34.9%; Score 942.5; DB 2; Length 459;
Best Local Similarity 38.7%; Pred. No. 2.4e-73;
Matches 190; Conservative 95; Mismatches 141; Indels 65; Gaps 8;
QY 35 KNYNPLRPVANDSOPLTVYFSLSLQIMDVDEKNQVLTNNIWLQMSWTDHYLQWNVSEY 94
Db 10 ERYNKLIRPAVNVKSSQVTTIGIKVSLAQISVNEREQIMTTNVLWTQETWTDYRLVWDPNEY 69
QY 95 PGVKTVPDQGIWPKDILLVNSADERDFTHTNLVNSGHCQYLPPIGFKSSCYIDV 154
Db 70 EGIKKLIRPQSHIWLDPDILVNNADGVTEVSFYCNVNSGTGDIITWLPALYKSALEV 129
QY 155 RWFPPDVQCHCKLKFGSWYGGWSLDLQMQE--ADISGIYPNGEWDLVGIPGKRSERFEC 212
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Db 130 RNFPPDQNCNTLKFRSWTYDRTELDTLVTSDPASRDDYTPSGEWDIVSLPGKNE----- 184
QY 213 CKEP-----YPOVTFVTRRRRTLYYGLNLLIPCVLISALALLVFLPADSGEKISLGTIV 268
Db 185 --DPNDLTLDITYDFVIRKRPFLFTINLIIIPCVLITSLAILVFLPSDCGKVTLCMSV 242
QY 269 LLSLVTFMILLVAEIMPATSDSVFLIAQYFASMTIIVGLSVVTVIVLQVHHHDPDGGKMP 328
Db 243 LLALIVFLLLISKIIVPTTSLAVPLIGLYKLMFTWLVTFISVTSVCLNVHHRSPSTHYMP 302
QY 329 KWTIVILLNWCWAFIRMKRPGEDKVRPACQKQRCRCLASVEMSAVAPPASNGNLLIYIG 368
Db 303 EWWKCVFLHKLPAFLIMRRPGRSNVRERFRKQKRSFSSHQ----- 344
QY 389 FRGLDGVHCVPTPDGSGVCGRMACSPTHDEHLHGGQPPEG-----DPDLAKIL 437
Db 345 -----DGSFLLTDDPGVCGAWRV-----GDLPEGSEFRQVRKVRHDDQVDEAL 369
QY 438 EEVRYIANFRQDESEAVCEWKFACVVDRLCLMAFVTTICTIGILMSAPNF----- 493
Db 390 DGVRFIAEHMKIETDDDEGIIDWKYVAMVIDRLFLWIFILVCVVGTLGLFVQ--PLFQSYN 448
QY 494 -----VEAVSKDF 501
Db 449 TPVAEEVYGD 459

RESULT 14
ACCH2N
nicotinic acetylcholine receptor alpha-2 chain precursor, neuronal - chicken
C;Species: Gallus gallus (chicken)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jul-2000
C;Accession: S00377
R;Nef, P.; Oneyser, C.; Alliod, C.; Couturier, S.; Ballivet, M.
EMBO J. 7, 595-601, 1988
A;Title: Genes expressed in the brain define three distinct neuronal nicotinic acetylcholine receptor subunit families: I, II, and III
A;Reference number: S00376; MUID:88283624; PMID:3267226
A;Accession: S00377
A;Molecule type: DNA
A;Residues: 1-528 <NEF>
A;Cross-references: EMBL:X07339; NID:g62792; PIDN:CAB59645.1; PID:g6136914
C;Genetics:
A;Introns: 21/1; 73/3; 88/3; 125/2; 487/3
C;Superfamily: acetylcholine receptor
C;Keywords: Glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane;
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-528/Product: nicotinic acetylcholine receptor alpha-2 chain #status predicted <NA>
F;241-264/Domain: transmembrane #status predicted <TM1>
F;272-290/Domain: transmembrane #status predicted <TM2>
F;306-327/Domain: transmembrane #status predicted <TM3>
F;502-520/Domain: transmembrane #status predicted <TM4>
F;54,104/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;158-172,222-223/Disulfide bonds: #status predicted

Query Match 34.8%; Score 941.5; DB 1; Length 528;
Best Local Similarity 38.0%; Pred. No. 3.5e-73;
Matches 201; Conservative 85; Mismatches 174; Indels 69; Gaps 10;
QY 8 WLAL-----AASLLHVSILQGEFQRLKYLKELVKNVPLRPPVANDSOPLTVYFSLSLQIMD 64
Db 13 VMCFTVLOAATREOKQPHGFAEDRLFKHLFTGYNWRSPVPNTSDVIVKFGSLIAQLID 72
QY 65 VDEKNQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVPFPDQGIWPKDILLVNSADERDPA 124
Db 73 VDEKNQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVPFPDQGIWPKDILLVNSADERDPA 132
QY 125 THTNVLVNSGHCQYLPPIGFKSSCYIDVRFPDQVCHCKLKFGSWYGGWSLDLQMQE 184
Db 133 THMTKAHLFSGKVKVPPALYKSSCSIDVTFYFPDQNCMKKFGSWTDYKAKIDLENNE 192
QY 185 --ADISGIYPNGEWDLVGIPGKRSERFECCKEYKPYDVTFTVTRRETLIYGLNLLIPCV 242
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Db 193 HVDLKDYESEWAIINAGRYNKKYDCCTEIPDITTFYVIRRLFLFYTNLIIPCL 252
QY 243 LISALALVFLPADSGEKISGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFA 298
Db 253 LISCLTVLVPSPDCGKVTLCISVLLSLTVFLLITETIPSTSLVPLIGEVYLL 307
QY 303 IVGLSVVTVIVLYHHDDPDGKMPKTRVILLNCAWFLRMKR-----PGEDKV--- 353
Db 313 FVTLIIITVFNHHRSPSTHTWPHVRSFLLGIFRWLEPMKRPPLLPAGTTGQYD 372
QY 354 RPACQKORRCSLAS-----VMSAVAPPPASNGNLLYIGRGLDG 394
Db 373 PGTRLSTSCRLVDDVDKWEEREEEBEEREEKAYPSRPSG-----GSGG 424
QY 395 VHCVTPTDGVVCGMACSPFTHDEHLLHGGQPE-----GD-----PDLAKILEE 439
Db 425 TQC-----HYSCERQAGKAS-----GGPAPQVPLKGEYVGSQGLTSLPSIIRALEG 471
QY 440 VRYIANRFRCDSEAVCSWKFAACVDRCLCLMAFSVFIICTIGILM 488
Db 472 VQYIADHLRAEDAFSVKEDWKVAMVIDRIFLWFIIVCLLGTVGLFL 520

RESULT 15

A53956
nicotinic acetylcholine receptor alpha-3 chain precursor, neuronal - human
C:Species: Homo sapiens (man)
C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 20-Aug-1999
C:Accession: A53956; S21338
R:Milohovic, M.; Roses, A.D.
Exp. Neurol. 111, 175-180, 1991
A:Title: Expression of mRNAs in human thymus coding for the alpha3 subunit of a neuronal
A:Reference number: A53956, MUID:91114756; PMID:1989896
A:Accession: A53956
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-503 <MIH>
A:Cross-references: GB:M37981; NID:g189252; PIDN:AAA59942.1; PID:g189253
R:Anand, R.; Lindstrom, J.
submitted to the EMBL Data Library, June 1990
A:Description: Nucleotide sequence of the mature human nicotinic acetylcholine receptor
A:Reference number: S21338
A:Accession: S21338
A:Molecule type: mRNA
A:Residues: 30-503 <ANA>
A:Cross-references: EMBL:X53559; NID:g34985; PIDN:CAA37625.1; PID:g34986
C:Genetics:
A:Gene: GDB:CHRNA3
A:Cross-references: GDB:125219; OMIM:118503
A:Map position: 15q24-15q24
C:Superfamily: acetylcholine receptor
C:Keywords: neurotransmitter receptor

Query Match 34.8%; Score 940.5; DB 2; Length 503;
Best Local Similarity 37.6%; Pred. No. 4e-73;
Matches 192; Conservative 95; Mismatches 166; Indels 57; Gaps 8;

QY 4 SPGGV---WLALASLILHVSLOGEFQRLKYLKYNVPLRPVANDSQPLTVYFSLSL 60
Db 8 APGAVAPRLLLLSLLFPARASAEHRLFERLFEDYNEIIRPVANVSDPVIHFEVMS 67
QY 61 QIMDVDEKNQVLTNWLQMSWTDHYLQNVSEYGVKTVRFPDGOIWKPDILYNSADE 120
Db 68 QLVKQVDEVNQIMETNLWLKQIWNQYKLNWFSYDGGAEFMRVPAQKIWKPDIVLYNNAV 127
QY 121 RFDATFHTNVLNVSCHQYLPQGIKSSCYIDVRWFFDVQHCKLKPQGSWSYGGWSLDL 180
Db 128 DFQVDDKTKALKYTGVTWIPPAIFKSSCKIDVTYFPFDYQNCYTMKFGWSYDKAKIDL 187
QY 181 QM--QEADISGIYINGEWDLVGIPGKRSERYECKEYPDYFTVTMRRRTLYVGLNLL 238
Db 188 VLGSSMNLKQYWSGESWAIKAPGYKHDIKYNCCIEYDPDITYSLYIRRLPLFYTNLI 247

QY 239 IPCVLISALALLVFLPADSGEKISGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFA 298
Db 248 IPCLLIISFLTVLVFLPSDCGKVTLCISVLLSLTVFLLITETIPSTSLVPLIGEVYLL 307
QY 299 STMIIVGLSVVTVIVLYHHDDPDGKMPKTRVILLNCAWFLRMKRPGEDKVRPACQ 358
Db 308 FTMIFVTLSIVITVFLNVHYRTPTTHTMPSWVKTVFLNLLPRVMEWTRP----- 357
QY 359 HKQRCSLASVMSAVAPPPASNGNLLYIGRGLDGVHCVTPTDPS-----GVVCGMACS 413
Db 358 -----TSNEGNAQRPRLYGAE-----LSNLCFSRAESKGCKEGYPCQDGMCG 401
QY 414 PTHDEHL-----LHGGQPEG-----DPDLAKILEEVRYIANRFRCDSEEA 455
Db 402 YCHHRIKISFNLSANLTRSSSESVDVLSLSALSPEIKETKAIQSVKYIAENKQAQNEAKE 461
QY 456 VCSEWKFAACVDRCLCLMAFSVFIICTIG 485
Db 462 IQDDWKYVAMVIDRIFLW---VFTLVCTLG 488

Search completed: May 5, 2004, 15:32:01
Job time : 22 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2004, 15:31:33 ; Search time 49 Seconds
(without alignments)
2839.779 Million cell updates/sec

Title: US-09-703-951A-12

Perfect score: 2702

Sequence: 1 MRCSGGVWLAALAAALHVS.....TIGILMSAPNFVAVSKDFA 502

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1138120 seqs, 277189581 residues

Total number of hits satisfying chosen parameters: 1138120

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2702	100.0	502	9	US-09-892-985-8
2	2698	99.9	502	10	US-09-954-936-2
3	2697	99.8	502	15	US-10-434-364-4
4	2694	99.7	502	15	US-10-352-684A-56
5	2674	99.0	502	15	US-10-434-364-27
6	2546	94.2	502	15	US-10-434-364-10
7	2026	75.0	446	14	US-10-349-836-12
8	1258.5	48.6	501	9	US-09-303-232-6
9	1246	46.1	496	9	US-09-303-232-4
10	1159.5	42.9	770	9	US-09-303-232-2
11	1108.5	41.0	498	15	US-10-369-493-6415
12	1093.5	40.5	560	15	US-10-369-493-5169
13	1092	40.4	554	14	US-10-203-968-12
14	999	37.0	461	15	US-10-369-493-5084
15	963	35.6	622	9	US-09-941-179A-11

16	949	35.1	529	14	US-10-349-836-2	Sequence 2, Appli
17	947	35.0	622	9	US-09-941-179A-3	Sequence 3, Appli
18	945	35.0	542	15	US-10-369-493-6980	Sequence 6980, Ap
19	937	34.7	502	14	US-10-157-031-92	Sequence 92, Appli
20	936	34.6	504	14	US-10-349-836-4	Sequence 4, Appli
21	932.5	34.5	631	9	US-09-941-179A-7	Sequence 7, Appli
22	924.5	34.2	528	9	US-09-892-985-2	Sequence 2, Appli
23	920	34.0	627	14	US-10-349-836-6	Sequence 6, Appli
24	912	33.8	504	9	US-09-892-985-4	Sequence 4, Appli
25	885	32.8	498	14	US-10-349-836-18	Sequence 18, Appli
26	875.5	32.4	450	9	US-09-795-693-11	Sequence 11, Appli
27	875.5	32.4	450	14	US-10-156-239-11	Sequence 11, Appli
28	875.5	32.4	450	14	US-10-199-485-11	Sequence 11, Appli
29	871.5	32.3	450	15	US-10-312-088-38	Sequence 38, Appli
30	871.5	32.3	494	14	US-10-349-836-10	Sequence 10, Appli
31	871.5	32.3	494	15	US-10-303-198-2	Sequence 2, Appli
32	870	32.2	498	9	US-09-892-985-12	Sequence 12, Appli
33	870	32.2	627	9	US-09-892-985-6	Sequence 6, Appli
34	867.5	32.1	529	9	US-09-795-693-31	Sequence 31, Appli
35	867.5	32.1	529	14	US-10-156-239-31	Sequence 31, Appli
36	867.5	32.1	529	14	US-10-199-485-31	Sequence 31, Appli
37	865	32.0	502	9	US-09-892-985-10	Sequence 10, Appli
38	865	32.0	502	14	US-10-349-836-14	Sequence 14, Appli
39	846	31.3	457	14	US-10-157-031-28	Sequence 28, Appli
40	842	31.2	437	14	US-10-261-798-69	Sequence 69, Appli
41	838.5	31.0	468	15	US-10-369-493-5462	Sequence 5462, Ap
42	832	30.8	534	15	US-10-369-493-5029	Sequence 5029, Ap
43	803	29.7	449	14	US-10-199-995-2	Sequence 2, Appli
44	803	29.7	479	14	US-10-349-836-20	Sequence 20, Appli
45	799.5	29.6	479	14	US-10-203-968-11	Sequence 11, Appli

ALIGNMENTS

RESULT 1

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US-09-892-985-8
; Sequence 8, Application US/09892985
; Patent No. US20020111463A1
; GENERAL INFORMATION:
; APPLICANT: Eliot, Kathryn J.
; Ellis, Steven B.
; Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION NUMBER: US/09/892,985
; FILING DATE: 27-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/217,345
; FILING DATE: 21-DEC-98
; APPLICATION NUMBER: US 08/467,574
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/466,589,
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
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; REFERENCE/DOCKET NUMBER: 24735-9949B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-450-8400
; TELEFAX: 619-587-5360
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-892-985-8

Query Match 100.0%; Score 2702; DB 9; Length 502;
Best Local Similarity 100.0%; Pred. No. 4.4e-263;
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAALAAASLLHVSLOGEFORKLYKELVKNYNPLERPVANDSQPLTVYFSL 60
DB 1 MRCSPGGVWLAALAAASLLHVSLOGEFORKLYKELVKNYNPLERPVANDSQPLTVYFSL 60
QY 61 QIMDVDEKNQVLTINILQMSWTDHYLQNVSEYPGVKTVPDPGQIWKPDILLNSADE 120
DB 61 QIMDVDEKNQVLTINILQMSWTDHYLQNVSEYPGVKTVPDPGQIWKPDILLNSADE 120
QY 121 RFDATFHTNVLNVSCHCOYLPPIGFKSSCYIDVRWFFDVQHCCKLKFSGWSYGGW 180
DB 121 RFDATFHTNVLNVSCHCOYLPPIGFKSSCYIDVRWFFDVQHCCKLKFSGWSYGGW 180
QY 181 QMQRADISGYIPNGEWDLVGIPGKRSERFYECCKEPYDPVTFVTMRRRTLYYGLNLLIP 240
DB 181 QMQRADISGYIPNGEWDLVGIPGKRSERFYECCKEPYDPVTFVTMRRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFAST 300
DB 241 CVLISALALLVFLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIVGLSVVTVTVLYQHHDHDPGGMKPKWTRVILLNWCAMFLRMKRGEDKVRPACQHK 360
DB 301 MIIVGLSVVTVTVLYQHHDHDPGGMKPKWTRVILLNWCAMFLRMKRGEDKVRPACQHK 360
QY 361 QRCCLSLASVEMSAVAPPPASNGNLLYIGRGLDGVHCVPPTDPSGVVCGRMACSPTHDEHL 420
DB 361 QRCCLSLASVEMSAVAPPPASNGNLLYIGRGLDGVHCVPPTDPSGVVCGRMACSPTHDEHL 420
QY 421 LHGGQPPEGDPDLAKILEEVRYIANFRQCQDESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
DB 421 LHGGQPPEGDPDLAKILEEVRYIANFRQCQDESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 3
US-10-434-364-4
; Sequence 4, Application US/10434364
; Publication No. US20040009554A1
; GENERAL INFORMATION:
; APPLICANT: WANG, DAGUANG
; TITLE OF INVENTION: QM-7 AND QM-6 CELLS TRANSFECTED WITH MUTANT CELL
; TITLE OF INVENTION: SURFACE EXPRESSED CHANNEL RECEPTORS AND ASSAYS USING
; TITLE OF INVENTION: THE TRANSFECTED CELLS
; FILE REFERENCE: MEMORY-11
; CURRENT APPLICATION NUMBER: US/10/434,364
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 60/378,642
; PRIOR FILING DATE: 2002-05-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-434-364-4

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; REFERENCE/DOCKET NUMBER: 24735-9949B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-450-8400
; TELEFAX: 619-587-5360
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-892-985-8

Query Match 100.0%; Score 2702; DB 9; Length 502;
Best Local Similarity 100.0%; Pred. No. 4.4e-263;
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAALAAASLLHVSLOGEFORKLYKELVKNYNPLERPVANDSQPLTVYFSL 60
DB 1 MRCSPGGVWLAALAAASLLHVSLOGEFORKLYKELVKNYNPLERPVANDSQPLTVYFSL 60
QY 61 QIMDVDEKNQVLTINILQMSWTDHYLQNVSEYPGVKTVPDPGQIWKPDILLNSADE 120
DB 61 QIMDVDEKNQVLTINILQMSWTDHYLQNVSEYPGVKTVPDPGQIWKPDILLNSADE 120
QY 121 RFDATFHTNVLNVSCHCOYLPPIGFKSSCYIDVRWFFDVQHCCKLKFSGWSYGGW 180
DB 121 RFDATFHTNVLNVSCHCOYLPPIGFKSSCYIDVRWFFDVQHCCKLKFSGWSYGGW 180
QY 181 QMQRADISGYIPNGEWDLVGIPGKRSERFYECCKEPYDPVTFVTMRRRTLYYGLNLLIP 240
DB 181 QMQRADISGYIPNGEWDLVGIPGKRSERFYECCKEPYDPVTFVTMRRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFAST 300
DB 241 CVLISALALLVFLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIVGLSVVTVTVLYQHHDHDPGGMKPKWTRVILLNWCAMFLRMKRGEDKVRPACQHK 360
DB 301 MIIVGLSVVTVTVLYQHHDHDPGGMKPKWTRVILLNWCAMFLRMKRGEDKVRPACQHK 360
QY 361 QRCCLSLASVEMSAVAPPPASNGNLLYIGRGLDGVHCVPPTDPSGVVCGRMACSPTHDEHL 420
DB 361 QRCCLSLASVEMSAVAPPPASNGNLLYIGRGLDGVHCVPPTDPSGVVCGRMACSPTHDEHL 420
QY 421 LHGGQPPEGDPDLAKILEEVRYIANFRQCQDESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
DB 421 LHGGQPPEGDPDLAKILEEVRYIANFRQCQDESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 2
US-09-954-936-2
; Sequence 2, Application US/09954936
; Publication No. US20030073161A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Clark A.
; APPLICANT: Gopalakrishnan, Murali
; APPLICANT: McKenna, David G.
; APPLICANT: Monteggia, Lisa M.
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Sullivan, James P.
; APPLICANT: Touma, Edward
; APPLICANT: Abbott Laboratories
; TITLE OF INVENTION: A VARIANT HUMAN ALPHA 7 ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR SUBUNIT, AND METHODS OF PRODUCTION AND USES THEREOF
; FILE REFERENCE: 6017.US.01
; CURRENT APPLICATION NUMBER: US/09/954,936

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; SEQ ID NO 27
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Macaca mulatta
US-10-434-364-27

Query Match          99.0%; Score 2674; DB 15; Length 502;
Best Local Similarity 98.8%; Pred. No. 2.9e-260;
Matches 496; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MRCSPGGWLAASLLHVSLOGEFQRLYKELVNKNYPLRPPVANDSQPLTVYFSLIQMDV 65
Db 1 MRCSPGGWLAASLLHVSLOGEFQRLYKELVNKNYPLRPPVANDSQPLTVYFSLIQMDV 65
QY 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQNVSEYPGVKTVRFPDQGIWKPDIILYNSADERFDT 125
Db 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQNVSEYPGVKTVRFPDQGIWKPDIILYNSADERFDT 125
QY 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQNVSEYPGVKTVRFPDQGIWKPDIILYNSADERFDT 125
Db 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQNVSEYPGVKTVRFPDQGIWKPDIILYNSADERFDT 125
QY 121 RFDAFTHTNVLNSSGHCQYLPPIGIFKSSCYIDVRWFFDVQHCCKLFGSWSYGGWSLDL 180
Db 121 RFDAFTHTNVLNSSGHCQYLPPIGIFKSSCYIDVRWFFDVQHCCKLFGSWSYGGWSLDL 180
QY 181 QMGEADISGYIPSGEWDLVGIPGKRSERFYECCKEYPDVTFTVMRRRTLYYGLNLLIP 240
Db 181 QMGEADISGYIPSGEWDLVGIPGKRSERFYECCKEYPDVTFTVMRRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLGTITVLLSTVFMLLVAEIMPATSDSVPLIAQYFAST 300
Db 241 CVLISALALLVFLPADSGEKISLGTITVLLSTVFMLLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIVGLSVVTVTVLQYHHDDPGGKMPKWTIVLLNWCWFLMRKRPGEDEVKVPACQHK 360
Db 301 MIIVGLSVVTVTVLQYHHDDPGGKMPKWTIVLLNWCWFLMRKRPGEDEVKVPACQHK 360
QY 361 QRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPDPSGVVCGMACSPHDEHL 420
Db 361 QRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPDPSGVVCGMACSPHDEHL 420
QY 421 LHGGQPPGDDPLAKTILEEVRYIANFRQDSEAVCSWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPGDDPLAKTILEEVRYIANFRQDSEAVCSWKFAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFEAVSKDFA 502
Db 481 ICTIGILMSAPNFEAVSKDFA 502

RESULT 6
US-10-434-364-10
; Sequence 10, Application US/10434364
; Publication No. US20040009554A1
; GENERAL INFORMATION:
; APPLICANT: WANG, DAGUANG
; TITLE OF INVENTION: QM-7 AND Q7-6 CELLS TRANSFECTED WITH MUTANT CELL
; TITLE OF INVENTION: SURFACE EXPRESSED CHANNEL RECEPTORS AND ASSAYS USING
; FILE REFERENCE: MEMORY-11
; CURRENT APPLICATION NUMBER: US/10/434,364
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 60/378,642
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 10
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-434-364-10

Query Match          94.2%; Score 2546; DB 15; Length 502;
Best Local Similarity 93.8%; Pred. No. 2.3e-247;
Matches 466; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

QY 6 GGVWLAASLLHVSLOGEFQRLYKELVNKNYPLRPPVANDSQPLTVYFSLIQMDV 65
Db 6 GGVWLAASLLHVSLOGEFQRLYKELVNKNYPLRPPVANDSQPLTVYFSLIQMDV 65
QY 66 DEKNQVLTNNIWLQMSWTDHYLQNVSEYPGVKTVRFPDQGIWKPDIILYNSADERFDT 125
Db 66 DEKNQVLTNNIWLQMSWTDHYLQNVSEYPGVKTVRFPDQGIWKPDIILYNSADERFDT 125
QY 126 PHTNVLNVSNGHCQYLPPIGIFKSSCYIDVRWFFDVQHCCKLFGSWSYGGWSLDLQMOEA 185
Db 126 PHTNVLNVSNGHCQYLPPIGIFKSSCYIDVRWFFDVQHCCKLFGSWSYGGWSLDLQMOEA 185
QY 186 DISGYIPNGEWDLVGIPGKRSERFYECCKEYPDVTFTVMRRRTLYYGLNLLIPCVLIS 245
Db 186 DISGYIPNGEWDLVGIPGKRSERFYECCKEYPDVTFTVMRRRTLYYGLNLLIPCVLIS 245
QY 246 ALALLVFLPADSGEKISLGTITVLLSTVFMLLVAEIMPATSDSVPLIAQYFASTMIIVG 305
Db 246 ALALLVFLPADSGEKISLGTITVLLSTVFMLLVAEIMPATSDSVPLIAQYFASTMIIVG 305
QY 306 LSVVTVTVLQYHHDDPGGKMPKWTIVLLNWCWFLMRKRPGEDEVKVPACQHKRRCS 365
Db 306 LSVVTVTVLQYHHDDPGGKMPKWTIVLLNWCWFLMRKRPGEDEVKVPACQHKRRCS 365
QY 366 LASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPDPSGVVCGMACSPHDEHLHGGQ 425
Db 366 LASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPDPSGVVCGMACSPHDEHLHGGQ 425
QY 426 PPEGDDPLAKTILEEVRYIANFRQDSEAVCSWKFAACVVDRLCLMAFSVFTI 485
Db 426 PPEGDDPLAKTILEEVRYIANFRQDSEAVCSWKFAACVVDRLCLMAFSVFTI 485
QY 486 ILSAPNFEAVSKDFA 502
Db 486 ILSAPNFEAVSKDFA 502

RESULT 7
US-10-349-836-12
; Sequence 12, Application US/10349836
; Publication No. US20030138911A1
; GENERAL INFORMATION:
; APPLICANT: Elliott, Kathryn J.
; Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION NUMBER: US/10/349,836
; FILING DATE: 23-Jan-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,451A
; FILING DATE: June 7, 1996
; APPLICATION NUMBER: 08/484,722
; FILING DATE: 07-Jun-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9370B
; TELECOMMUNICATION INFORMATION:
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; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 446 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-349-836-12

Query Match      75.0%; Score 2026; DB 14; Length 446;
Best Local Similarity 86.3%; Pred. No. 5.2e-195;
Matches 433; Conservative 4; Mismatches 9; Indels 56; Gaps 35;

QY 1 MRCSPGGVWLAALASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSLSL 60
Db 1 MRCSPGGVWAAAS-----HVS-QGEFQK-YKE-VKNYNP-ERPVANDSQP-TVIFS---S 48

QY 61 QIMDVDEKQVLTNIWQMSWTDHYLQMNVSYPGVKTVRPPDQGIWKPDILLYNSADE 120
Db 49 QIMDVDEKQV--TTNIW-QMSWTDHY-QMNVSYPGVKTVRPPDQGIWKPDILLYNSADE 103

QY 121 RPDATHNVLNVSCHQVLPDGIKSSCYIDVRWPPFDVQCHCKLFGSWSYGGHSLDL 180
Db 104 RPDATHNVLNVSCHQVLPDGIKSSCYIDVRWPPFDVQCHCKLFGSWSYGGHSLDL 158

QY 181 QMGEADISGYPNGEMDLVGIPGKRSEFYECCKEPPDVFTVTMRRRTLYYGLNLLIP 240
Db 159 QMGEADISGYPNGEMD-VGIPGKRSEFYECCKEPPDVFTVTMRRRTLYYGLNLLIP 213

QY 241 CVLISALALAVFLPADSGEKISLGITVLLSLVFMLLVAEIMPATSDSVPLIAQYFAS 300
Db 214 CVISAA-----VFPADSGEKIS-GITV---SVFM--VAEIMPATSDSVPLIAQYFAS 260

QY 301 MIIVGLSVVTVIVLYQHHDHDPGGKMPKWTIVILLNWCANFLMKRPGEDKVRPACQHK 360
Db 261 MIIVG-SVVTVIV-QYHHDDPGGKMPKWTIV--NWCANF-RMKRPGEDKVRPACQHK 315

QY 361 QRCCLASVEMSAVAPPASNGMLLYIGFGLDGVHCVPTPDGSGVCGMACGPTHDEHL 420
Db 316 QRCCLASVEMSAVAPPASNGN--YIGFRG-DGVHCVPTPDGSGVCGMACGPTHDEH- 370

QY 421 LHGGQPPEGDPDLAKILLEVRYIANRPRCODESAVCSEWKFAACVVDRLCLMAFSVFTI 480
Db 371 -HGQPPEGDPD-AKI-EEVRYIANRPRCODESAVCSEWKFAACVVDRLCLMAFSVFTI 425

QY 481 ICTIGILMSAPNFVAVSKDFA 502
Db 426 ICTIGI-MSAPNFVAVSKDFA 446

RESULT 8
US-09-303-232-6
; Sequence 6, Application US/09303232A
; Patent No. US20020006657A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; TITLE OF INVENTION: Nucleic Acids which encode
; FILE REFERENCE: Le A 33 020-Foreign Countries
; CURRENT APPLICATION NUMBER: US/09/303,232A
; EARLIER FILING DATE: 1999-04-30
; EARLIER FILING DATE: 1998-05-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1

Query Match      46.1%; Score 1246; DB 9; Length 496;
Best Local Similarity 46.0%; Pred. No. 2.6e-116;
Matches 240; Conservative 86; Mismatches 126; Indels 70; Gaps 6;

QY 4 SPGGVWLAALASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSLSLQIM 63

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; SEQ ID NO 6
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Heliothis virescens
US-09-303-232-6

Query Match      46.6%; Score 1258.5; DB 9; Length 501;
Best Local Similarity 48.6%; Pred. No. 1.5e-117;
Matches 250; Conservative 75; Mismatches 138; Indels 51; Gaps 7;

QY 10 LALAASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSLSLQIMDVDEKN 69
Db 8 LALLA-LLPVSEQGPKHEKLLNALLANVTNLERPVANSEPLEVFGLTQIQLIIDVEKN 66

QY 70 QVLTNIMLQMSWTDHYLQMNVSYPGVKTVRPPDQGIWKPDILLYNSADERPDATFTN 129
Db 67 QLLITNIMLSLEWNDYNLRWNSDYGGVKDLRITPKLWKPDVLMYNSADEGDFGTQTN 126

QY 130 VLVNSGHCQVLPDGIKSSCYIDVRWPPFDVQCHCKLFGSWSYGGHSLDLQWQE---AD 186
Db 127 VVVRSGGSLYVPPGIFKSTCKMDIAWFFDDQCHDMKFGSWTYDGNQLDLVKDBAGGD 186

QY 187 ISGYIPNGEMDLVGIPGKRSEFYECCKEPPDVFTVTMRRRTLYYGLNLLIPCVLISA 246
Db 187 LSDFITNGEWYLIHGMKKNYTYACCPYVDVFTIMRRRTLYYFNLLIVPCVLIS 246

QY 247 LALLVFLPADSGEKISLGITVLLSLVFMLLVAEIMPATSDSVPLIAQYFASITMIVGL 306
Db 247 MALLGFTLPDPSGKLTIGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMPVAS 306

QY 307 SVVTVIVLYQHHDHDPGGKMPKWTIVILLNWCANFLMKRPGEDKVRPACQHKQRCSL 366
Db 307 SVVTVVVLNLYHRTADIHEMPQWIKSVFLQMLPWILRMSRPGKIKTRKTMNTMRREL 366

QY 367 ASVEMSAVA-----PPP---ASNGMLLYIGFGLDGVHCVPTPDGSGVVC 407
Db 367 ELKERSKSLANVLIDDDFRHGPPPPNSTAGNL-----GPGC 407

QY 408 G-----RMACSPTHDEHLHGQPPGDPDLAKILLEVRYIANRPRCODESAVCSEW 460
Db 408 SIPTDFRRSFVRPSTMEDV--GGGLGSHRHLHLILRELOFTIARMKADBEAELISDW 465

QY 461 KFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494
Db 466 KFAAMVVDRCLEFVFTLTITVAVLLSAPHII 499

RESULT 9
US-09-303-232-4
; Sequence 4, Application US/09303232A
; Patent No. US20020006657A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; TITLE OF INVENTION: Nucleic Acids which encode
; FILE REFERENCE: Le A 33 020-Foreign Countries
; CURRENT APPLICATION NUMBER: US/09/303,232A
; EARLIER FILING DATE: 1999-04-30
; EARLIER FILING DATE: 1998-05-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1

Query Match      46.1%; Score 1246; DB 9; Length 496;
Best Local Similarity 46.0%; Pred. No. 2.6e-116;
Matches 240; Conservative 86; Mismatches 126; Indels 70; Gaps 6;

QY 4 SPGGVWLAALASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSLSLQIM 63

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Db 12 APAGLLLLCLLWPRGARGVGEKLLHLLDHYNVLEPVVNESDPLQLSGLTLMQII 71
QY 64 DVDEKXQVLTNINWLOMSWTDHYLQWNVSEYGVKTVRPDPQIQWKPDIILVNSADERD 123
Db 72 DVDEKXQVLTNINWLOMSWTDHYLQWNVSEYGVKTVRPDPQIQWKPDIILVNSADERD 131
QY 124 ATFTNVLNNSGHCQYLPFGKSSCYIDVRWFPDQVHCKLKFSGWSYGGWSLDLQMQ 183
Db 132 STYPTNVVRNNGSCLYVPPGFKSKCKIDITWFPDDQRCCKMFGSWYDGVQLDLQ 191
QY 184 E---ADISYIPNGEWDLVGIPKRSERYECCKEYPDVTVTVMRRRTLYGMLLPCVLI 244
Db 192 DEGGDISFVNGEWELIGVPGKREIYVNCCEPYDITFAVWIRKRTLYFFNLIVP 251
QY 241 CVLISALALLVLLPADSGEKISLGLTIVLLSLVFMLLVAEIMPATSDSVPLIAQYFAST 300
Db 252 CVLIASALLGFTLPDPGSEKLSLGLTIVLLSLVFMLLVAEIMPATSDSVPLIAQYFAST 311
QY 301 MIIVGLSVVTVIVLYQHHPDGGKMPKRWTRVILLNWCANFLMRKRPGEKVRPACQHK 360
Db 312 MFWASVSVSTIILINYYHRAUTHESMDWIRCVELYWLPWLRMSRPG----- 360
QY 361 QRCCLASVMSAVAPPPASNGNLLYIGRGLDGVHCVPDPDGSVVGCRMACSPTH---- 416
Db 361 -----SATTPPPAR-----VPPPPDLERRSKSLLANVLD 392
QY 417 -DEHLLH-----GGQPPG-----DPLAKILERVYIANRFRQDE 452
Db 393 IDDFRHPQAOQCCRYGGEENGAGLAHSCFGVDYLSLILKEIRVITQMRKDE 452
QY 453 SEAVCSWEKFAACVDRCLMAFSVFTIICITIGILMSAPNFV 494
Db 453 DADISRDKKFAAMVVDRLCLIFTLEIATLAVLLSAPHIM 768

RESULT 10

US-09-303-232-2
; Sequence 2, Application US/09303232A
; Patent No. US20020006657A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; TITLE OF INVENTION: Nucleic Acids which encode
; TITLE OF INVENTION: Insect acetylcholine receptor subunits
; FILE REFERENCE: Le A 33 020-Foreign Countries
; CURRENT APPLICATION NUMBER: US/09/303,232A
; CURRENT FILING DATE: 1999-04-30
; EARLIER APPLICATION NUMBER: DE 198 19 829.9
; EARLIER FILING DATE: 1998-05-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-303-232-2

Query Match 42.9%; Score 1159.5; DB 9; Length 770;
Best Local Similarity 45.1%; Pred No. 2.7e-107;
Matches 237; Conservative 82; Mismatches 115; Indels 91; Gaps 12;

QY 8 VWLAAALLHVSLOGEFO-RKLYKELVKNYNPLERPVANDSQPLTVYFSLQLQIMVDY 67
Db 297 IYINLSAK---VCLAGYHEKRLHLLDLPYNTLERPVLESPLQLSGLTLMQIIDYDE 353
QY 68 KNOVLTTNWLQMSWTDHYLQWNVSEYGVKTVRPDPQIQWKPDIILVNSADERD 127
Db 354 KNOVLTTNWLQMSWTDHYLQWNVSEYGVKTVRPDPQIQWKPDIILVNSADERD 413
QY 128 TNVLNNSGHCQYLPFGKSSCYIDVRWFPDQVHCKLKFSGWSYGGWSLDLQMQE--- 184
Db 414 TNVVRNNGSCLYVPPGFKSKCKIDITWFPDDQRCCKMFGSWYDGVQLDLQQLDGTG 473

QY 185 ADISYIPNGEWDLVGIPKRSERYECCKEYPDVTVTVMRRRTLYGMLLPCVLI 244
Db 474 GDISSYLVNGEWELIGVPGKREIYVNCCEPYDITFAVWIRKRTLYFFNLIVP 533
QY 245 SALALLVLLPADSGEKISLGLTIVLLSLVFMLLVAEIMPATSDSVPLIAQYFAST 304
Db 534 ASMALLGFTLPDPGSEKLSLGLTIVLLSLVFMLLVAEIMPATSDSVPLIAQYFAST 581
QY 305 GLSVVVTVIVLYQHHPDGGKMPKRWTRVILLNWCANFLMRKRPGEKVRP-ACQHKQR 363
Db 582 -----WIRIVFLCMLPWLRMSRPG-----RPLILEFFPTTP 612
QY 364 CSLASVE-----MSAVAPPPASNGNLLY-----IGFRGLDGVHCVP-TP 401
Db 613 CSDDTSERKQHLSDVELKERSKSLLANVLDIDDDFH-----NCRPMTPGTLPENPAF 668
QY 402 -----DSGVV-----CGRMACSPTHDEHLLHGGQPPGDPDLAKILEEVYIANRFR 449
Db 669 YRTVYGGDDGSGIGPIGSTMPDAVTH-----HTCIKSTVEYELGLILKEIRFITDQLRK 723
QY 450 QDESEAVCSWEKFAACVDRCLMAFSVFTIICITIGILMSAPNFV 494
Db 724 DDECNDIANDKFAAMVVDRLCLIFTLEIATLAVLLSAPHIM 768

RESULT 11

US-10-369-493-6415
; Sequence 6415, Application US/10369493
; Publication No. US2003023675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6415
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6415

Query Match 41.0%; Score 1108.5; DB 15; Length 498;
Best Local Similarity 44.6%; Pred No. 1.9e-102;
Matches 226; Conservative 77; Mismatches 167; Indels 37; Gaps 7;

QY 10 LALAASLLHVSLOGEFO-RKLYKELVKNYNPLERPVANDSQPLTVYFSLQLQIMVDY 68
Db 6 LLISCAILAAPTLGLSGLQERLYEDLMRNYNLPERPVANHSEPVTVHLKVALQIIDYDEK 65
QY 69 NQVLTTNWLQMSWTDHYLQWNVSEYGVKTVRPDPQIQWKPDIILVNSADERD 128
Db 66 NQVYVNAWLDYTNWYDCAEYGNITDVRFPAGKIWKPDVLLNSVDTFNDSYQ 125
QY 129 NVLVNNSGHCQYLPFGKSSCYIDVRWFPDQVHCKLKFSGWSYGGWSLDLQMQE--D 186
Db 126 NMIVSYGLVHWVPPGFKSKCKIDIQWFFDEQCKCFKFGSWYDGVQLDLQATG 185
QY 187 ISGYIPNGEWDLVGIPKRSERYECCKEYPDVTVTVMRRRTLYGMLLPCVLI 246
Db 186 ISEYISNGEWALPLTTVERNEKFDCCPEYDPVDFVHFLHMRRTLYGFLNIMPCILTL 245
QY 247 LALLVLLPADSGEKISLGLTIVLLSLVFMLLVAEIMPATSDSVPLIAQYFAST 306
Db 246 MTLGLFTLPDPAGEKITLIQTIVLLSICFFLSIVSEMSPPTSEAVPLIGIFFTCMIVVTA 305

QY 307 SVVTVTVILQYHHDPDGGKMPKWTVRVILLNWCWFLRMKRPBGDKVRPACQKQRCSL 366
 DB 306 STVFTVTVLNLHRTPTETHDMPWTRNLLLYWIPWILRMKRP-----HNLTVASL 356
 QY 367 ASVEMSAVAPPPASNGNLLYIGFGLDGVHCVPPDS-----GVVCGRMAC 412
 DB 357 PSL-----FSTKPNRHSLSLRNIK--DNEHSLSRANSFDACRLNQVIMTQSVNGLTSL 410
 QY 413 SPTHDEHLLHGGQPPGDPD-----LAKILEEYVIANRFRCDSEAVSCSEWKFACVV 467
 DB 411 GSIPSTWISNGTTDVSQQATLLILHRIYHELKIVTKRMIEGDKESQACNNWKFAMVV 470
 QY 468 DRCLMAFSVFTIICIGILMSAPNFV 494
 DB 471 DRCLXYVFTIIVSTIGIFWSAPYLV 497

RESULT 12
 US-10-369-493-5169
 ; Sequence 5169, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; PRIOR FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 5169
 ; LENGTH: 560
 ; TYPE: PRT
 ; ORGANISM: Caenorhabditis elegans
 US-10-369-493-5169

Query Match 40.5%; Score 1093.5; DB 15; Length 560;
 Best Local Similarity 40.8%; Pred. No. 7.4e-101;
 Matches 227; Conservative 93; Mismatches 156; Indels 81; Gaps 9;

QY 10 LALAASLI-----HVSILQSGFQRLKLYKELVKNYNPLERPVANDSOPLTVYFSLSLQI 62
 DB 8 LVLVSILLTWETKCSKVIWTGDHERRLYAKLAENYKRLARPVRNESEAVVLLGMDYQOI 67
 QY 63 MDVDEKQVLTNNIWLQMSWTDHYLQWNVSEYFGVKTVPDQGIWKPDILLYNSADERF 122
 DB 68 LDIDEKHQIMNSVNLMSWTDHYLTWDPSEFGNIKEVRLPINNIWKPDVLLYNSVDQOF 127
 QY 123 DATFTNNVLNSGHCQYLPDGIKSSCYIDVRWFPDVQHCCLKFSGWSYSGWSDILOM 182
 DB 128 DSTMPVNAVLYTGNVTWIPPAIRSSCAIDIAFPDQHCCTKFGSWTYSGFTDLIN 187
 QY 183 QEADISGYTPNGEWDLVGIPGKRSERFYECCKEPPYDVTFTVMRRRTLYYGLNLLIPC 242
 DB 188 TTISPATYKNGEWELLGTSQRSIFFYECCKEPPYDVTFTVIRRTLYYGFNLLPCN 247
 QY 243 LISALLVFLPADSGEKISIGITVLLSLTVFMLVAEIMPATSDSVPLIAQYFASMTI 302
 DB 248 LISSALLSFTLPADCGEKLNGVTIFMSLCVPMVIAEAMPQTSDALPLIQIFSCIMF 307
 QY 303 IVGLSVVTVTVILQYHHDPDGGK--MPKWTVRVILLNWCWFLRMKRPBGDKVRPACQH-- 359
 DB 308 QVGSVAVTVIALNFHRSPEQYKPMNKFLLKLLGMLPTLLGMRPDLVLSVHGAYHA 367
 QY 360 ----KQRCCLASVEMSAVAPPASNGNLLYIGFGLD----- 393
 DB 368 SDNKKQRYLIEVERHILTRP---NGN-----GHSVAVDKAVHLDLSTGNPHSDAKKSSFS 420

QY 394 -----GVHCVPTP-----DSGV---VCGRMACSPTHDEHLLHGGQPPGDP----- 431
 DB 421 PKRTSASIMGWGLPTQMGALDSSINKYCTKTVRPLENGSATINHKSSPQINPINNN 480
 QY 432 -----DLAKILEEYVIANRFRCDSEAVSCSEWKFACVADRCLCMAP 475
 DB 481 NIYKCANNOKTQPDREHFRHILNELRVISARVKEEAMHALQADWMPASFVRVDRVCLAF 540
 QY 476 SVFTIICIGILMSAPN 492
 DB 541 SAFELFMCTAISYNAPH 557

RESULT 13
 US-10-203-968-12
 ; Sequence 12, Application US/10203968
 ; Publication No. US20030186370A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Commonwealth Scientific and Industrial Research Organisation
 ; APPLICANT: TROWELL, Stephen Charles
 ; APPLICANT: EAST, Peter David
 ; APPLICANT: LIAO, Chunyan
 ; APPLICANT: DUMANCIC, Mira Maria
 ; TITLE OF INVENTION: 5HT3 Receptors of Nematodes, Polynucleotide Molecules Encoding ;
 ; TITLE OF INVENTION: Antagonists Thereof
 ; FILE REFERENCE: 050179-0106
 ; CURRENT APPLICATION NUMBER: US/10/203,968
 ; CURRENT FILING DATE: 2002-08-15
 ; PRIOR APPLICATION NUMBER: PCT/AU01/00150
 ; PRIOR FILING DATE: 2001-02-15
 ; PRIOR APPLICATION NUMBER: P05634
 ; PRIOR FILING DATE: 2000-02-15
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 12
 ; LENGTH: 554
 ; TYPE: PRT
 ; ORGANISM: Caenorhabditis elegans
 US-10-203-968-12

Query Match 40.4%; Score 1092; DB 14; Length 554;
 Best Local Similarity 40.6%; Pred. No. 1e-100;
 Matches 224; Conservative 95; Mismatches 159; Indels 74; Gaps 8;

QY 8 VVLAASLLHVSLSQGEFQRLKLYKELVKNYNPLERPVANDSOPLTVYFSLSLQIMDYDE 67
 DB 7 IGIAFPFALFRVITWGDHERRLYAKLAENYKRLARPVRNESEAVVLLGMDYQOILDIDE 66
 QY 68 KNOVLTTNWLQMSWTDHYLQWNVSEYFGVKTVPDQGIWKPDILLYNSADERFATFH 127
 DB 67 KQIMNSVNLMSWTDHYLTWDPSEFGNIKEVRLPINNIWKPDVLLYNSVDQDFSTWP 126
 QY 128 TNVLVNSGHCQYLPDGIKSSCYIDVRWFPDVQHCCLKFSGWSYSGWSDILOMQEADI 187
 DB 127 VNAVLYTGNVTWIPPAIRSSCAIDIAFPDQHCCTKFGSWTYSGFTDLINTTISP 186
 QY 188 SCYIPNGEWDLVGIPGKRSERFYECCKEPPYDVTFTVMRRRTLYYGLNLLIPCULISAL 247
 DB 187 ATYKNGEWELLGTSQRSIFFYECCKEPPYDVTFTVIRRTLYYGFNLLPCMLISSL 246
 QY 248 ALLVFLPADSGEKISIGITVLLSLTVFMLVAEIMPATSDSVPLIAQYFASMTIIVGLS 307
 DB 247 ALLSFTLPADCGEKLNGVTIFMSLCVPMVIAEAMPQTSDALPLIQIFSCIMFQVGS 306
 QY 308 VVVTVTVILQYHHDPDGGK--MPKWTVRVILLNWCWFLRMKRPBGDKVRPACQH-----K 360
 DB 307 VVATVIALNFHRSPEQYKPMNKFLLKLLGMLPTLLGMRPDLVLSVHGAYHSDNKK 366
 QY 361 QRCCLASVEMSAVAPPASNGNLLYIGFGLD----- 393
 DB 367 KQRYLIEVERHILTRP---NGN-----GHSVAVDKAVHLDLSTGNPHSDAKKSSPSPKRTS 419
 QY 394 -----GVHCVPTP-----DSGV---VCGRMACSPTHDEHLLHGGQPPGDP----- 431

Db 420 ASIMGWGLPTQMGALDSSINKYCTKVRPLENGSATINKHSSPQINNNNNIYKC 479
QY 432 -----DLAKILEEYRIANRFRCDSEAVCEWKFPAACVDRCLCMAFVSFTI 480
Db 480 ANNOKTQEDRHFHILNELRVISARVKEEAMHALQADWMFASRVVDVRCFLAFSAFLF 539
QY 481 ICTIGILMSAPN 492
Db 540 MCTAISYNAPH 551
RESULT 14
US-10-369-493-5084
; Sequence 5084, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10 (52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5084
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5084
Query Match 37.0%; Score 999; DB 15; Length 461;
Best Local Similarity 39.8%; Pred. No. 1.9e-91;
Matches 197; Conservative 96; Mismatches 146; Indels 56; Gaps 8;
QY 12 LAASLHVSI--QGEF--ORLYKELVKNYNPLRPVANDSOPLYVYSLSLQIMVDENK 69
Db 10 LSLVITHSNLDCGSAETKLFDTLLKGYNPLRPVQNSQPLEVKIKLFLQQILYDVENK 69
QY 70 QVLTITNWLQMSWTDVLOKNVSEYPCGVKVRPP--DGLWKPDILLXNSADERDATEH 127
Db 70 QIVSVNAWLSYTFWFDHKLQWEPKYGIGQIRFPGSSDHLWKPDVLLYNSAAEDFSTFX 129
QY 128 TNVLVNSSGHCQYLPFGIFKSSCYIDVRFPFDVQHCKLFGWSYSGWSLDLQM----- 182
Db 130 SNLLTYHTGTVMIPGVLKFCQLDVTWFPDQVCEMFGSWTFHGYAIDLQIDDDTN 189
QY 183 --QADISGYIPNGEWDLVGIPGRSERFYECCKEYPDVTFTVMRRRTLYGLNLIP 240
Db 190 GTQSMDSLTVLNGEWQVISTNAKRVSYKCCPEYPTVNYLHRRRTLYYGFNLIP 249
QY 241 CVLISALALVFLPADSGEKISLIGITVLLSLTFVMLLVAEIMPATSDSVPLIAQYFAS 300
Db 250 SLLISLMAILGFMFPDAGEKITLEVILLAIIVFLSNVSEMTPTSEAVPLIGVFFS 309
QY 301 MIIVGLSVVTVTVIYQVHHDDPGDKMPKTRVILLNWCAMFLRMKRPGEKVPACQHK 360
Db 310 MLVVSASVVTIVLNLHFRSADSHENPNLVRRLVLEPLPWLLEFMSRPGYKFKV----- 363
QY 361 QRRCLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVCGRMACSPTHDEH 419
Db 364 -----ANV-----IDSTDKMPKPKPNLDCNLPSNAGYEAQ 395
QY 420 LLHGQOPGEGDPLAKILEEVRIANRFRCDSEAVCEWKFPAACVVDRLCMAFVSFT 479
Db 396 ILL-----LHVSHTELRRVVAFTNKEEHDRIQTDRFAMVVDRACLLLFTVFI 445
QY 480 ICTIGILMSAPNFV 494

Db 446 VISILAIMSAPHII 460
RESULT 15
US-09-941-179A-11
; Sequence 11, Application US/09941179A
; Patent No. US20020146765A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; TITLE OF INVENTION: Acetylcholine receptor subunits
; FILE REFERENCE: Le A 34 821
; CURRENT APPLICATION NUMBER: US/09/941,179A
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: DE 100 42 177.6
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 11
; LENGTH: 622
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Modified alpha
; OTHER INFORMATION: 4 subunit of the chicken nicotinic acetylcholine
; OTHER INFORMATION: receptor
US-09-941-179A-11
Query Match 35.6%; Score 963; DB 9; Length 622;
Best Local Similarity 34.5%; Pred. No. 1.2e-87;
Matches 210; Conservative 90; Mismatches 185; Indels 124; Gaps 9;
QY 4 SPGGVWLALASLL-----HVSLLQGEFQRLKYKELVKNYNPLRPVANDSOPLYVYSLSL 59
Db 6 SKGNLALLLCAISIFPAFGHVETRAHAERLLKLFSGYNKNSRPVANISDVVLVRFGLSI 65
QY 60 LQIMVDENKQVLTNWLQMSWTDVLOKNVSEYPCGVKTRFPDQGWKPDILLYNSAD 119
Db 66 AQLIDVDENKQVLTNWLQMSWTDVLOKNVSEYPCGVKTRFPDQGWKPDILLYNSAD 125
QY 120 ERFDATFHNVLVNSSGHCQYLPFGIFKSSCYIDVRFPFDVQHCKLFGWSYSGWSLD 179
Db 126 GDFAVTHLTAKHLFYDGRKKNWPPALYKSSCSIDVTFFDFDQDQCNKMGKSGWTYDKAKID 185
QY 180 L--QMGADISGYIPNGEWDLVGIPGRSERFYECCKEYPDVTFTVMRRRTLYGLNL 237
Db 186 LVSMHSHVDLSEFYTSVENDLLEVPVRNKEFYTCDEPYLDITFIRRLPFLFTYINL 245
QY 238 LTPCVLISALALVFLPADSGEKISLIGITVLLSLTFVMLLVAEIMPATSDSVPLIAQYF 297
Db 246 IIPCLLISCLTVLVFLPSECGEKITLCISVLLSLVFLLLITEIIPSTSLVPLIGEYL 305
QY 298 ASTMIIVGLSVVTVTVIYQVHHDDPGDKMPKTRVILLNWCAMFLRMKRPGE----- 349
Db 306 LFTWIFVTLISIIITVFLVNLVHHSRPTHMPDWRVRVFLDIVPRLLFMKRPSTVDKNCCK 365
QY 350 -----EDKVRPACQHKOR 362
Db 366 LIESMHKLTNSPRLWSETDMEPNFTTSSPSPQSNSEFPTSSCAHLEEPKMPCKSPSG 425
QY 363 RCLSLASVE---MSAVAPPPA-----SNGNLL-----YIGFRGLD 393
Db 426 QYSLMHEPFPQVTCSSPKPSCHEPLSDTOTTSISGRSLSVQOYSPNKPTEGSIKRSRS 485
QY 394 GVHCVPFPDGSVCGRMACSP-----HDEHLH-----GGQPEG----- 429
Db 486 IQCYLQEDSSQTNHSHSSASPASQCHLNEEQPHKPHQCKCKRKGAAAGTPTQGSKSH 545
QY 430 -----DPLAKILEEVRIANRFRCDSEAVCEWKFPAACVVDRLCMAFVSFT 479
Db 546 SNKGEHLVMSPALKLAVEGVHYIADHLRAEDADFSVKEDWKYVAMVIDRFLMNFIIVC 605
QY 480 ICTIGILM 488

Db 606 LLGTVGLFL 614
 :: |:::

Search completed: May 5, 2004, 15:37:26
Job time : 50 secs

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OM protein - protein search, using sw model

Run on: May 5, 2004, 15:28:53 ; Search time 22 Seconds
(without alignments)
1178.011 Million cell updates/sec

Title: US-09-703-951A-12
Perfect score: 2702
Sequence: 1 KRCSFGVWLAASILHVS.....TIGILMSAFVFAVSKDFA 502

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A COMB.pdp.*
2: /cgn2_6/ptodata/2/iaa/5B COMB.pdp.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2702	100.0	502	2	US-08-466-589-8
2	2702	100.0	502	2	US-08-700-636-8
3	2702	100.0	502	3	US-08-467-574-8
4	2702	100.0	502	4	US-09-217-345-8
5	2702	100.0	502	4	US-08-487-596-12
6	2702	100.0	502	4	US-09-892-985-8
7	2698	99.9	502	4	US-08-771-737-2
8	2698	99.9	502	4	US-09-954-936-2
9	2544	94.2	502	1	US-08-278-635B-7
10	2544	94.2	502	3	US-08-464-258B-7
11	2544	94.2	502	3	US-08-471-961-7
12	2544	94.2	502	4	US-09-345-109C-7
13	2026	75.0	446	4	US-08-660-451A-12
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18	949	35.1	529	1	US-08-496-855A-2
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21	947	35.0	510	1	US-08-278-635B-4
22	947	35.0	510	3	US-08-471-961-4
23	947	35.0	510	4	US-09-345-109C-4
24	944.5	35.0	511	3	US-08-464-258B-4
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27	924.5	34.2	528	2	US-08-700-636-2

28	924.5	34.2	528	3	US-08-467-574-2	Sequence 2, Appli
29	924.5	34.2	528	4	US-09-217-345-2	Sequence 2, Appli
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31	920	34.0	627	4	US-08-660-451A-6	Sequence 6, Appli
32	912	33.8	504	2	US-08-466-589-4	Sequence 4, Appli
33	912	33.8	504	2	US-08-700-636-4	Sequence 4, Appli
34	912	33.8	504	3	US-08-467-574-4	Sequence 4, Appli
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43	898	33.2	497	3	US-08-471-961-5	Sequence 5, Appli
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45	891	33.0	627	4	US-08-487-596-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-08-466-589-8
; Sequence 8, Application US/08466589
; Patent No. 5837489
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClaim
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,589
; FILING DATE: June 5, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: March 8, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9950
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-466-589-8

Query Match 100.0% Score 2702; DB 2; Length 502;
Best Local Similarity 100.0%; Pred. No. 1.4e-272;
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPPTDPSGVVCGRMACSPTHDEHL 420
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Db 481 ICTIGILMSAPNFVEAVSKDFA 502
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RESULT 2

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US-09-700-636-8
; Sequence 8, Application US/08700636
; Patent No. 5910582
; GENERAL INFORMATION:
; APPLICANT: Eliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 16-JUL-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen B.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9368
; TELECOMMUNICATION INFORMATION:
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TELEPHONE: 619-546-4737
TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-700-636-8
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Query Match 100.0%; Score 2702; DB 2; Length 502;
Best Local Similarity 100.0%; Pred. No. 1.4e-272;
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQMNVSYPGVKTVRFDPGQIWKPDILLYNSADE 120
Qy 121 RFDAFTHTNVLVNSGHCQYLPPGIFKSSCYIDVRWPFDDVQHCCKLFGWSYSGWSL 180
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Db 301 MIIVGLSVVVTVIVLQYHHHPDGGKMPKTRVILLNWCWFLMRKRPGEKVRPACQHK 360
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RESULT 3

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US-08-467-574-8
; Sequence 8, Application US/08467574
; Patent No. 6022704
; GENERAL INFORMATION:
; APPLICANT: Eliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
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OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA: US/08/467,574
APPLICATION NUMBER: US/08/467,574
FILING DATE: June 5, 1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: March 8, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9949
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 502 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-467-574-8

Query Match 100.0%; Score 2702; DB 3; Length 502;
Best Local Similarity 100.0%; Pred. No. 1.4e-272; Indels 0; Gaps 0;
Matches 502; Conservative 0; Mismatches 0;
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Db 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTFVMLLVAEIMPATSDSVPLIAQYFAS 300
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Db 301 MIIVGLSVVTVIVLQYHHDPDGGKMPKTRVILLNWCANFLMRKRGEDKVRPACQHK 360
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RESULT 4

US-09-217-345-8
; Sequence 8, Application US/09217345
; Patent No. 6303753
; GENERAL INFORMATION:
; APPLICANT: Elliott, Kathryn J.

APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McAuliffe
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/217,345
FILING DATE: 21-DEC-98
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,574
FILING DATE: 05-JUN-95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/466,589,
FILING DATE: 05-JUN-95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-MAR-93
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24735-9949B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-450-8400
TELEFAX: 619-587-5360
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 502 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-217-345-8

Query Match 100.0%; Score 2702; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 1.4e-272; Indels 0; Gaps 0;
Matches 502; Conservative 0; Mismatches 0;
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Db 1 MRCSPGGVWLAALASLLHVSLLQGEFQKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
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Db 61 QIMDVDEKNQVLTNIWLSQSWTDHYLQWNVSEYPGKTVRFPDQGIWKPDILLYNSADE 120
Qy 121 RFDAFTHTNVLVNSGHCQYLPPGIFKSSCYDVRWFFPDVQHCCLKFGWSYSGWSL 180
Db 121 RFDAFTHTNVLVNSGHCQYLPPGIFKSSCYDVRWFFPDVQHCCLKFGWSYSGWSL 180
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Db 181 QMOEADISGYIPNGEWDLVGIPGKRSEYFECCKEYDPDVTFTVMRRRTLYYGLNLLIP 240
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Db 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTFVMLLVAEIMPATSDSVPLIAQYFAS 300
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DB 361 QRCCLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPPTDPSGVVCGMACSPHDEHL 420
QY 421 LHGGOPPEGDPLAKILEEVRYIANRFRCDSEAVCSEWKFACVWDRCLCLMAFSVFTI 480
DB 421 LHGGOPPEGDPLAKILEEVRYIANRFRCDSEAVCSEWKFACVWDRCLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 5

US-08-487-596-12
; Sequence 12, Application US/08487596
; Patent No. 6440681
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND
; TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NEURONAL
; TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,596
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US94/02447
; FILING DATE: 08-MAR-1994
; APPLICATION NUMBER: US 08/149,503
; FILING DATE: 08-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,154
; FILING DATE: 30-NOV-1992
; APPLICATION NUMBER: US 07/504,455
; FILING DATE: 03-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9951
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-487-596-12

Query Match

100.0%; Score 2702; DB 4; Length 502;

Best Local Similarity 100.0%; Pred. No. 1.4e-272;
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRCSPGGWLAALASLLHVSLOGEFOKLYKELVKNYNPLERPVPANDSQPLTVVFSLSLL 60
DB 1 MRCSPGGWLAALASLLHVSLOGEFOKLYKELVKNYNPLERPVPANDSQPLTVVFSLSLL 60
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DB 181 QMOEADISGYIPNGEWDLVGIPGKSERFYECCKEYPDVTFTVMRRRTLYYGLNLLIP 240
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QY 481 ICTIGILMSAPNFVEAVSKDFA 502
DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 6

US-09-892-985-8
; Sequence 8, Application US/09892985
; Patent No. 6664375
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/892,985
; FILING DATE: 27-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/217,345
; FILING DATE: 21-DEC-98
; APPLICATION NUMBER: US 08/467,574
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/466,589,
; FILING DATE: 05-JUN-95

APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-MAR-93
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24735-9949B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-450-8400
TELEFAX: 619-587-5360
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 502 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-892-985-8

Query Match 100.0%; Score 2702; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 1.4e-272; Indels 0; Gaps 0;
Matches 502; Conservative 0; Mismatches 0;

Qy	1	MRCSPGGVWLALAAASLLHVSLSQGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSL	60
Db	1	MRCSPGGVWLALAAASLLHVSLSQGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSL	60
Qy	61	QIMDVDEKQVLTNTIWLQMSWTDHYLQWNVSEYGVKTVRFDDGQIWKPDILLYNSADE	120
Db	61	QIMDVDEKQVLTNTIWLQMSWTDHYLQWNVSEYGVKTVRFDDGQIWKPDILLYNSADE	120
Qy	121	RFDAFTNTVNVSSGHCQYLPFGIFKSSCYIDVRWFPFDVQHCCLKFGSWSYGSWLSLD	180
Db	121	RFDAFTNTVNVSSGHCQYLPFGIFKSSCYIDVRWFPFDVQHCCLKFGSWSYGSWLSLD	180
Qy	181	QMQEADISGYPNGEWDLVGIPGKRSEYECCKEYPDVTFTVMRRRTLYYGLNLLIP	240
Db	181	QMQEADISGYPNGEWDLVGIPGKRSEYECCKEYPDVTFTVMRRRTLYYGLNLLIP	240
Qy	241	CVLISALALLVFLPADSGEKISLGIITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAS	300
Db	241	CVLISALALLVFLPADSGEKISLGIITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAS	300
Qy	301	MIIVGLSVVTVIVLQYHHDDPDGGMKPKTRVILLNWCAMFLMKRPGEDKVPACQHK	360
Db	301	MIIVGLSVVTVIVLQYHHDDPDGGMKPKTRVILLNWCAMFLMKRPGEDKVPACQHK	360
Qy	361	QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVCGMACSPTHDEHL	420
Db	361	QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVCGMACSPTHDEHL	420
Qy	421	LHGQPPGPDPLAKILLEVRYIANRFRQDESEAVCSEWKFACVVDRLCLMAFSVFTI	480
Db	421	LHGQPPGPDPLAKILLEVRYIANRFRQDESEAVCSEWKFACVVDRLCLMAFSVFTI	480
Qy	481	ICTIGILMSAPNFVEAVSKDFA 502	
Db	481	ICTIGILMSAPNFVEAVSKDFA 502	

RESULT 7

US-08-771-737-2

Sequence 2, Application US/08771737

Patent No.: 6323000

GENERAL INFORMATION:

APPLICANT: Briggs, Clark A.

APPLICANT: Gopalakrishnan, Murali

APPLICANT: McKenna, David G.

APPLICANT: Monteggia, Lisa M.

APPLICANT: Roch, Jean-Marc

APPLICANT: Sullivan, James P.

APPLICANT: Touma, Edward

APPLICANT: Abbott Laboratories
TITLE OF INVENTION: A VARIANT HUMAN ALPHA 7 ACETYLCHOLINE
RECEPTOR SUBUNIT, AND METHODS OF PRODUCTION AND USES THEREOF
FILE REFERENCE: 6017 US 01
CURRENT APPLICATION NUMBER: US/08/771,737
CURRENT FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 502
TYPE: PRT
ORGANISM: homo sapien
US-08-771-737-2

Query Match 99.9%; Score 2698; DB 4; Length 502;
Best Local Similarity 99.8%; Pred. No. 3.7e-272; Indels 0; Gaps 0;
Matches 501; Conservative 0; Mismatches 1;

Qy	1	MRCSPGGVWLALAAASLLHVSLSQGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSL	60
Db	1	MRCSPGGVWLALAAASLLHVSLSQGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSL	60
Qy	61	QIMDVDEKQVLTNTIWLQMSWTDHYLQWNVSEYGVKTVRFDDGQIWKPDILLYNSADE	120
Db	61	QIMDVDEKQVLTNTIWLQMSWTDHYLQWNVSEYGVKTVRFDDGQIWKPDILLYNSADE	120
Qy	121	RFDAFTNTVNVSSGHCQYLPFGIFKSSCYIDVRWFPFDVQHCCLKFGSWSYGSWLSLD	180
Db	121	RFDAFTNTVNVSSGHCQYLPFGIFKSSCYIDVRWFPFDVQHCCLKFGSWSYGSWLSLD	180
Qy	181	QMQEADISGYPNGEWDLVGIPGKRSEYECCKEYPDVTFTVMRRRTLYYGLNLLIP	240
Db	181	QMQEADISGYPNGEWDLVGIPGKRSEYECCKEYPDVTFTVMRRRTLYYGLNLLIP	240
Qy	241	CVLISALALLVFLPADSGEKISLGIITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAS	300
Db	241	CVLISALALLVFLPADSGEKISLGIITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAS	300
Qy	301	MIIVGLSVVTVIVLQYHHDDPDGGMKPKTRVILLNWCAMFLMKRPGEDKVPACQHK	360
Db	301	MIIVGLSVVTVIVLQYHHDDPDGGMKPKTRVILLNWCAMFLMKRPGEDKVPACQHK	360
Qy	361	QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVCGMACSPTHDEHL	420
Db	361	QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVCGMACSPTHDEHL	420
Qy	421	LHGQPPGPDPLAKILLEVRYIANRFRQDESEAVCSEWKFACVVDRLCLMAFSVFTI	480
Db	421	LHGQPPGPDPLAKILLEVRYIANRFRQDESEAVCSEWKFACVVDRLCLMAFSVFTI	480
Qy	481	ICTIGILMSAPNFVEAVSKDFA 502	
Db	481	ICTIGILMSAPNFVEAVSKDFA 502	

RESULT 8

US-09-954-936-2

Sequence 2, Application US/09954936

Patent No. 6683157

GENERAL INFORMATION:

APPLICANT: Briggs, Clark A.

APPLICANT: Gopalakrishnan, Murali

APPLICANT: McKenna, David G.

APPLICANT: Monteggia, Lisa M.

APPLICANT: Roch, Jean-Marc

APPLICANT: Sullivan, James P.

APPLICANT: Touma, Edward

APPLICANT: Abbott Laboratories

TITLE OF INVENTION: A VARIANT HUMAN ALPHA 7 ACETYLCHOLINE

RECEPTOR SUBUNIT, AND METHODS OF PRODUCTION AND USES THEREOF

FILE REFERENCE: 6017 US 01

CURRENT APPLICATION NUMBER: US/09/954,936

CURRENT FILING DATE: 2001-09-18

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; PRIOR APPLICATION NUMBER: 08/771,737
; PRIOR FILING DATE: 1996-12-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 502
; TYPE: PRT
; ORGANISM: homo sapien
US-09-954-936-2

Query Match      99.9%; Score 2698; DB 4; Length 502;
Best Local Similarity 99.8%; Pred. No. 3,7e-272;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGGWLAASLLHVSLSQGEFORKLYKELVKNYNPLRPVANDSQPLTVYFSLSL 60
DB 1 MRCSPGGWLAASLLHVSLSQGEFORKLYKELVKNYNPLRPVANDSQPLTVYFSLSL 60

QY 61 QIMVDKKNQVLTNIWLQSWTDHYLQNVSEYPGKTVRPPDGGQIKWPKDILLYNSADE 120
DB 61 QIMVDKKNQVLTNIWLQSWTDHYLQNVSEYPGKTVRPPDGGQIKWPKDILLYNSADE 120

QY 121 RFDATEHTNVLNNSGHCQYLPPIKSSCYIDVRWFPFDVQHCCKLKFGSWSYGWSL 180
DB 121 RFDATEHTNVLNNSGHCQYLPPIKSSCYIDVRWFPFDVQHCCKLKFGSWSYGWSL 180

QY 181 QMOEADISGVIENGWDVIGIPKRSERFVECKEYPDVFTVTMRRRTLYYGLNLLIP 240
DB 181 QMOEADISGVIENGWDVIGIPKRSERFVECKEYPDVFTVTMRRRTLYYGLNLLIP 240

QY 241 CVLISALALVFLPADSGEKISIGITVLLSLTFVLLVAEIMPATSDSVPLIAQYFAST 300
DB 241 CVLISALALVFLPADSGEKISIGITVLLSLTFVLLVAEIMPATSDSVPLIAQYFAST 300

QY 301 MIIVGLSVVTVIVLVQHHHDPDGGKMPKTRVILLNCAWFLMRKRPGEKVRPACQHK 360
DB 301 MIIVGLSVVTVIVLVQHHHDPDGGKMPKTRVILLNCAWFLMRKRPGEKVRPACQHK 360

QY 361 QRCSLASVMSAVAPPASGNLLYIGFRLDGVCVPTPDSGVVCGRMACSPTHDEHL 420
DB 361 QRCSLASVMSAVAPPASGNLLYIGFRLDGVCVPTPDSGVVCGRMACSPTHDEHL 420

QY 421 LHGQPEPDPDLAKILEEVRYIANRFRCDSEAVCSWKFAACVVDRLCLMAFSVFTI 480
DB 421 LHGQPEPDPDLAKILEEVRYIANRFRCDSEAVCSWKFAACVVDRLCLMAFSVFTI 480

QY 481 ICTGILMSAPNFVEAVSKDFA 502
DB 481 ICTGILMSAPNFVEAVSKDFA 502

RESULT 9
US-08-278-635B-7
; Sequence 7, Application US/08278635B
; Patent No. 5683912
; GENERAL INFORMATION:
; APPLICANT: ELGOYHEN, ANA BELEN
; APPLICANT: JOHNSON, DAVID S.
; APPLICANT: BOULTER, JAMES R.
; APPLICANT: HEINEMANN, STEPHEN F.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
; TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY CARY WARE & FREIDENRICH
; STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/278,635B
; FILING DATE: 21-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: REITER, STEPHEN E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9771
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-677-1409
; TELEFAX: 619-677-1465
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-278-635B-7

Query Match      94.2%; Score 2544; DB 1; Length 502;
Best Local Similarity 93.8%; Pred. No. 4e-256;
Matches 466; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

QY 6 GGVWLAASLLHVSLSQGEFORKLYKELVKNYNPLRPVANDSQPLTVYFSLSLQIMDV 65
DB 6 GGVWLAASLLHVSLSQGEFORKLYKELVKNYNPLRPVANDSQPLTVYFSLSLQIMDV 65

QY 66 DEKNQVLTNIWLQSWTDHYLQNVSEYPGKTVRPPDGGQIKWPKDILLYNSADERFAT 125
DB 66 DEKNQVLTNIWLQSWTDHYLQNVSEYPGKTVRPPDGGQIKWPKDILLYNSADERFAT 125

QY 126 FHTNVLNNSGHCQYLPPIKSSCYIDVRWFPFDVQHCCKLKFGSWSYGWSL 185
DB 126 FHTNVLNNSGHCQYLPPIKSSCYIDVRWFPFDVQHCCKLKFGSWSYGWSL 185

QY 186 DISGYIPNGEWDVIGIPKRSERFVECKEYPDVFTVTMRRRTLYYGLNLLIPCVLIS 245
DB 186 DISGYIPNGEWDVIGIPKRSERFVECKEYPDVFTVTMRRRTLYYGLNLLIPCVLIS 245

QY 246 ALALLYFLPADSGEKISIGITVLLSLTFVLLVAEIMPATSDSVPLIAQYFASTMIIVG 305
DB 246 ALALLYFLPADSGEKISIGITVLLSLTFVLLVAEIMPATSDSVPLIAQYFASTMIIVG 305

QY 306 LSVVVTVIVLVQHHHDPDGGKMPKTRVILLNCAWFLMRKRPGEKVRPACQHKORRCS 365
DB 306 LSVVVTVIVLVQHHHDPDGGKMPKTRVILLNCAWFLMRKRPGEKVRPACQHKORRCS 365

QY 366 LASVMSAVAPPASGNLLYIGFRLDGVCVPTPDSGVVCGRMACSPTHDEHLHGQ 425
DB 366 LASVMSAVAPPASGNLLYIGFRLDGVCVPTPDSGVVCGRMACSPTHDEHLHGQ 425

QY 426 PPSGDDPLAKILEEVRYIANRFRCDSEAVCSWKFAACVVDRLCLMAFSVFTI 485
DB 426 PPSGDDPLAKILEEVRYIANRFRCDSEAVCSWKFAACVVDRLCLMAFSVFTI 485

QY 486 ILMSAPNFVEAVSKDFA 502
DB 486 ILMSAPNFVEAVSKDFA 502

RESULT 10
US-08-464-258B-7
; Sequence 7, Application US/08464258B
; Patent No. 6013766
; GENERAL INFORMATION:
; APPLICANT: ELGOYHEN, ANA BELEN
; APPLICANT: JOHNSON, DAVID S.
; APPLICANT: BOULTER, JAMES R.
; APPLICANT: HEINEMANN, STEPHEN F.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
; TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
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Db 486 ILMSAPNFVEAVSKDFA 502

RESULT 11

US-08-471-961-7

Sequence 7, Application US/08471961

Patent No. 6100046

GENERAL INFORMATION:

APPLICANT: ELGOYHEN, ANA BELEN

APPLICANT: JOHNSON, DAVID S.

APPLICANT: BOULTER, JAMES R.

APPLICANT: HEINEMANN, STEPHEN F.

TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL

TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: GRAY CARY WARE & FREIDENRICH

STREET: 4365 EXECUTIVE DRIVE, SUITE 1600

CITY: SAN DIEGO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 92121

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/471,961

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/278,635

FILING DATE: 21-JUL-1994

ATTORNEY/AGENT INFORMATION:

NAME: REITER, STEPHEN E.

REGISTRATION NUMBER: 31,192

REFERENCE/DOCKET NUMBER: P41 9771

TELEPHONE: 619-677-1409

TELEFAX: 619-677-1465

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 502 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-471-961-7

Query Match 94.2%; Score 2544; DB 3; Length 502;

Best Local Similarity 93.8%; Pred. No. 4e-256;

Matches 466; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

QY 6 GGWVLAALAAALLHVSLOGEFORKLYKELVKYNPLERPVANDSPLTYVYFSLSLQIMDV 65

Db 6 GGIWLAALAAALLHVSLOGEFORRLLYKELVKYNPLERPVANDSPLTYVYFSLSLQIMDV 65

QY 66 DEKNQVLTNIWLQMSWTDHYLQNMSEYPGVKVTRPDGQIWKPDILLYNSADERFDT 125

Db 66 DEKNQVLTNIWLQMSWTDHYLQNMSEYPGVKVTRPDGQIWKPDILLYNSADERFDT 125

QY 126 FHTNVLVNSSGHCQYLPPIGIFKSSCYIDVRFPDVOHCKLKFGSWSYGGWSLDLQMOEA 185

Db 126 FHTNVLVNASSGHCQYLPPIGIFKSSCYIDVRFPDVOHCKLKFGSWSYGGWSLDLQMOEA 185

QY 186 DISGYIPNGEWDLVGIPGRSERFEYECCKEYPDVFTVTWRRRTLYYGLNLLIPCVLIS 245

Db 186 DISSYIPNGEWDLVGIPGRNEKEFEYECCKEYPDVFTVTWRRRTLYYGLNLLIPCVLIS 245

QY 246 ALALVFLPADSGEKISLIGITVLLSLTFVFMVAIMPATSDSVPLIAQYFASFTMIIVG 305

Db 246 ALALVFLPADSGEKISLIGITVLLSLTFVFMVAIMPATSDSVPLIAQYFASFTMIIVG 305

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: GRAY CARY WARE & FREIDENRICH LLP

STREET: 4365 EXECUTIVE DRIVE, SUITE 1600

CITY: SAN DIEGO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 92121

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/464,258B

FILING DATE: 06/05/95

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/278,635

FILING DATE: 21-JUL-1994

ATTORNEY/AGENT INFORMATION:

NAME: REITER, STEPHEN E.

REGISTRATION NUMBER: 31,192

REFERENCE/DOCKET NUMBER: P41 9989

TELEPHONE: 619-677-1409

TELEFAX: 619-677-1465

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 502 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-464-258B-7

Query Match 94.2%; Score 2544; DB 3; Length 502;

Best Local Similarity 93.8%; Pred. No. 4e-256;

Matches 466; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

QY 6 GGWVLAALAAALLHVSLOGEFORKLYKELVKYNPLERPVANDSPLTYVYFSLSLQIMDV 65

Db 6 GGIWLAALAAALLHVSLOGEFORRLLYKELVKYNPLERPVANDSPLTYVYFSLSLQIMDV 65

QY 66 DEKNQVLTNIWLQMSWTDHYLQNMSEYPGVKVTRPDGQIWKPDILLYNSADERFDT 125

Db 66 DEKNQVLTNIWLQMSWTDHYLQNMSEYPGVKVTRPDGQIWKPDILLYNSADERFDT 125

QY 126 FHTNVLVNSSGHCQYLPPIGIFKSSCYIDVRFPDVOHCKLKFGSWSYGGWSLDLQMOEA 185

Db 126 FHTNVLVNASSGHCQYLPPIGIFKSSCYIDVRFPDVOHCKLKFGSWSYGGWSLDLQMOEA 185

QY 186 DISGYIPNGEWDLVGIPGRSERFEYECCKEYPDVFTVTWRRRTLYYGLNLLIPCVLIS 245

Db 186 DISSYIPNGEWDLVGIPGRNEKEFEYECCKEYPDVFTVTWRRRTLYYGLNLLIPCVLIS 245

QY 246 ALALVFLPADSGEKISLIGITVLLSLTFVFMVAIMPATSDSVPLIAQYFASFTMIIVG 305

Db 246 ALALVFLPADSGEKISLIGITVLLSLTFVFMVAIMPATSDSVPLIAQYFASFTMIIVG 305

QY 306 LSVWTVTVLVLYHHDDPGGKPKVTRVILLNWCWFLRMKBPGEKVPACQKHORCS 365

Db 306 LSVWTVTVLVLYHHDDPGGKPKVTRVILLNWCWFLRMKBPGEKVPACQKHORCS 365

QY 366 LASVEMSAVAPPASNGNLLYTGFRGLDGVHCVPTPDGSGVCGRMACSPTHDEHLHGQ 425

Db 366 LASVELSAGAGPTNGNLLYTGFRLEGHCAVPTPDGSGVCGRLACSPTHDEHLMGAH 425

QY 426 PPEGPDALILEEVRYIANFRQDSEAVSEWKFPAACVVDRLCLMAFSFTIICITG 485

Db 426 PSDGPDALAKILEEVRYIANFRQDSEAVSEWKFPAACVVDRLCLMAFSFTIICITG 485

QY 486 ILMSAPNFVEAVSKDFA 502

Db 49 QIMDVDEKQV-TTNIW-QMSWDHY-QMNVSEYPGVKTFRFPDQIWKPD1--YNSADE 103
Qy 121 RFDATFTNVLNVSCHGCVLPFGIFKSSCYIDVRWEPFDVQCKLFGSWSYGGWLDL 180
Db 104 RFDATFTNV-VNSSGHCOY-PPGIFKSSCYIDVRWEPFDVQCK-KEGSWSYGGWS--D 158
Qy 181 QMOBADI SGYPNGEWDLVGPGRKSRFYECCKEPYDPDVTFTVMRRRTLYYGLNLLIP 240
Db 159 QMOBADI SGYPNGEWDLVGPGRKSRFYECCKEPYDPDVTFTVMRRRTLYYGLNLLIP 213
Qy 241 CVLISALALLVFLPADSGEKISIGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFAS 300
Db 214 CVISAA-----VFPADSGEKIS-GITV---STVFM--VAEIMPATSDSVPLIAQYFAS 260
Qy 301 MIIIVGLSVVTVIYVQHHDDPDGCKMPKTRVILLNWCWFLRMKPGEDKVRPACQHK 360
Db 261 MIIIVG-SVVTVIYV-QXHHDDPDGCKMPKTRVILLNWCWFLRMKPGEDKVRPACQHK 315
Qy 361 QRRCSLASVMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSDGVVCGRMACSPTHDEHL 420
Db 316 QRRCS-ASVMSAVAPPASNGN--YIGFRG-DGVHCVPTPDSDGVVCGRMACSPTHDEH- 370
Qy 421 LHGOQPEGDDLAKEVRYIANRFRCDSEAVCSEWKFACVDRCLMAFSVFTI 480
Db 371 -HGQPEGDD-KEVRYIANRFRCDSEAVCSEWKFACVDRCLMAFSVFTI 446
Qy 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 426 ICTIGI-MSAPNFVEAVSKDFA 446

RESULT 14
US-08-278-635B-8
; Sequence 8, Application US/08278635B
; Patent No. 5683912
; GENERAL INFORMATION:
; APPLICANT: ELGOYHEN, ANA BELEN
; APPLICANT: JOHNSON, DAVID S.
; APPLICANT: BOULTER, JAMES R.
; APPLICANT: HEINEMANN, STEPHEN F.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY CARY WARE & FREIDENRICH LLP
; STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/278,635B
; FILING DATE: 21-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: REITER, STEPHEN E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9771
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-677-1409
; TELEFAX: 619-677-1465
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 511 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-278-635B-8
Query Match 67.4%; Score 1820.5; DB 1; Length 511;
Best Local Similarity 69.0%; Pred. No. 9.5e-181;
Matches 343; Conservative 56; Mismatches 93; Indels 5; Gaps 4;
Qy 8 VMLAASLLHVSLOGEFORKLYKELVKNYNPIERPVPANDSQPITVTFSLQIIMDVDE 67
Db 16 LWASLFLSPFKVSOQSSQRLRYDLNRYNRLERPVPANDSQPITVTFSLQIIMDVDE 75
Qy 68 KNQVLTNINLQSWTDHLYQNVSEYPGVKTFRFPDQIWKPD1LYNLSADREFDATEH 127
Db 76 KNQVLTNINLQSWTDHLYQNVSEYPGVKTFRFPDQIWKPD1LYNLSADREFDATEH 135
Qy 128 TNVLNVSCHGCVLPFGIFKSSCYIDVRWEPFDVQCKLFGSWSYGGWLDLQMOBADI 187
Db 136 TNVLNVSCHGCVLPFGIFKSSCYIDVRWEPFDVQCKLFGSWSYGGWLDLQMOBADI 195
Qy 188 SGYPNGEWDLVGPGRKSRFYECCKEPYDPDVTFTVMRRRTLYYGLNLLIPCVLISAL 247
Db 196 SNTYISNGEWDLVGPGRKSRFYECCKEPYDPDVTFTVMRRRTLYYGLNLLIPCVLISGL 255
Qy 248 ALLVFLPADSGEKISIGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFASIMVIGLS 307
Db 256 ALLVFLPADSGEKISIGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFASIMVIGLS 315
Qy 308 VVTVIYVQHHDDPDGCKMPKTRVILLNWCWFLRMKPGEDKVRP-ACQHK--QRRC 364
Db 316 VVTVIYVQHHDDPDGCKMPKTRVILLNWCWFLRMKPGEDKVRP-ACQHK--QRRC 374
Qy 365 SLASVMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSDGVVCGRMACSPTHDEHLGG 424
Db 375 SLKNTENNVLPGHQSNGNMIY-SYHTMENPCCPQNNDLGSKGKITCPLSEDNEHVQKK 433
Qy 425 QPPEGDDLAKEVRYIANRFRCDSEAVCSEWKFACVDRCLMAFSVFTI 484
Db 434 ALMDTIPVIVKILEVOFIAMRFKQDEGEICSEWKFACVDRCLMAFSVFTI 493
Qy 485 GILMSAPNFVEAVSKDFA 501
Db 494 TILMSAPNFVEAVSKDFA 510
RESULT 15
US-08-464-258B-8
; Sequence 8, Application US/08464258B
; Patent No. 6013766
; GENERAL INFORMATION:
; APPLICANT: ELGOYHEN, ANA BELEN
; APPLICANT: JOHNSON, DAVID S.
; APPLICANT: BOULTER, JAMES R.
; APPLICANT: HEINEMANN, STEPHEN F.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY CARY WARE & FREIDENRICH LLP
; STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,258B
; FILING DATE: 06/05/95
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/278,635

Wed May 12 09:51:14 2004

Search completed: May 5, 2004, 15:32:37
Job time : 24 secs

DR N-PSDB; AAV12197.
 XX Human neuronal nicotinic acetylcholine receptor subunits and DNA - also
 PT transformed cells useful for screening cpds. which modulate activity of
 PT the receptor.
 XX
 PS Claim 7; Page 80-81; 99pp; English.
 XX
 PS The present sequence represents a human neuronal nicotinic acetylcholine
 CC receptor (NACHR) subunit. The cells expressing the alpha and/or beta
 CC NACHR subunits may be used in a method of screening compounds to identify
 CC any which modulate the activity of human neuronal NACHR. Subunit specific
 CC antibodies may be used to monitor the distribution and expression density
 CC of various subunits in normal vs diseased brain tissues. Testing of
 CC single receptor subunits or specific receptor subunit combinations with a
 CC variety of potential agonists or antagonists provides information with
 CC respect to the function and activity of the individual subunits and
 CC should lead to the identification and design of compounds that are
 CC capable of very specific interaction with one or more receptor subtypes.
 CC The resulting drugs should exhibit fewer unwanted side effects than drugs
 CC identified e.g. screening with cells that express a variety of subtypes
 XX
 SQ Sequence 502 AA;

Query Match 100.0%; Score 2702; DB 2; Length 502;
 Best Local Similarity 100.0%; Pred. No. 6.9e-264;
 Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAALASLHVSLQGEFORKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
 DB 1 MRCSPGGVWLAALASLHVSLQGEFORKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
 QY 61 QIMDVDEKNQVLTNNILQMSWTDHYLQWNVSEYGVKTVRFPDQGIWKPDIILYNSADE 120
 DB 61 QIMDVDEKNQVLTNNILQMSWTDHYLQWNVSEYGVKTVRFPDQGIWKPDIILYNSADE 120
 QY 121 RPDATFHTNVLVNSGHCQYLPPIGPKSSCYIDVRWFFPDVQHCCLKFGSWSYGWSL 180
 DB 121 RPDATFHTNVLVNSGHCQYLPPIGPKSSCYIDVRWFFPDVQHCCLKFGSWSYGWSL 180
 QY 181 QMGEADISGYIPNGEWDLVGIPGKSERFEYCKEPEYDVTFTVMRRRTLYYGLNLLIP 240
 DB 181 QMGEADISGYIPNGEWDLVGIPGKSERFEYCKEPEYDVTFTVMRRRTLYYGLNLLIP 240
 QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300
 DB 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300
 QY 301 MIIVGLSVVVTVIVLYQYHHDDPDGGMKPKWTRVILLNWCAMFLRMKRPGEKVRPACQHK 360
 DB 301 MIIVGLSVVVTVIVLYQYHHDDPDGGMKPKWTRVILLNWCAMFLRMKRPGEKVRPACQHK 360
 QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVTPTDPSGVVCGRMACSPHDEHL 420
 DB 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVTPTDPSGVVCGRMACSPHDEHL 420
 QY 421 LHGGQPPEGDPDLAKILEEVRYIANFRFCQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
 DB 421 LHGGQPPEGDPDLAKILEEVRYIANFRFCQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480

RESULT 2

AAW09025
 ID AAW09025 standard; protein; 502 AA.
 XX
 AC AAW09025;
 XX
 DT 09-APR-1997 (first entry)
 XX

DE Neuronal nicotinic acetylcholine receptor alpha-7 subunit.
 XX
 KW Neuronal nicotinic acetylcholine receptor; nAChR; neurotransmitter;
 KW ligand-gated receptor.
 XX
 OS Homo sapiens.
 XX
 PN MO9641876-A1.
 XX
 PD 27-DEC-1996.
 XX
 PF 07-JUN-1996; 96WO-US009775.
 XX
 PR 07-JUN-1995; 95US-00484722.
 XX
 PA (STBI-) SIBIA NEUROSCIENCES INC.
 XX
 PI Elliott KJ, Harpold MM;
 XX
 DR WPI; 1997-065463/06.
 DR N-PSDB; AAT48239.
 XX
 PT Nucleic acids encoding nicotinic acetylcholine receptor sub-units - used
 PT in screening to determine the effect of drugs on the receptor.
 XX
 PS Disclosure; Page 73-74; 108pp; English.
 XX
 CC The alpha-7 subunit (AAW09025) of the human neuronal nicotinic
 CC acetylcholine receptor (nAChR) can be expressed in transformed host cells
 CC carrying alpha-7 subunit DNA (see also AAT48239). Host cells, esp.
 CC mammalian cells or amphibian oocytes, expressing the recombinant alpha-7
 CC subunit, opt. in combination with other recombinant alpha and/or beta
 CC subunits (see also AAW09018-24, AAW09026-27), can be used to examine the
 CC function of human AChR and to identify cpds. that modulate its activity
 XX
 SQ Sequence 502 AA;

Query Match 100.0%; Score 2702; DB 2; Length 502;
 Best Local Similarity 100.0%; Pred. No. 6.9e-264;
 Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAALASLHVSLQGEFORKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
 DB 1 MRCSPGGVWLAALASLHVSLQGEFORKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
 QY 61 QIMDVDEKNQVLTNNILQMSWTDHYLQWNVSEYGVKTVRFPDQGIWKPDIILYNSADE 120
 DB 61 QIMDVDEKNQVLTNNILQMSWTDHYLQWNVSEYGVKTVRFPDQGIWKPDIILYNSADE 120
 QY 121 RPDATFHTNVLVNSGHCQYLPPIGPKSSCYIDVRWFFPDVQHCCLKFGSWSYGWSL 180
 DB 121 RPDATFHTNVLVNSGHCQYLPPIGPKSSCYIDVRWFFPDVQHCCLKFGSWSYGWSL 180
 QY 181 QMGEADISGYIPNGEWDLVGIPGKSERFEYCKEPEYDVTFTVMRRRTLYYGLNLLIP 240
 DB 181 QMGEADISGYIPNGEWDLVGIPGKSERFEYCKEPEYDVTFTVMRRRTLYYGLNLLIP 240
 QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300
 DB 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300
 QY 301 MIIVGLSVVVTVIVLYQYHHDDPDGGMKPKWTRVILLNWCAMFLRMKRPGEKVRPACQHK 360
 DB 301 MIIVGLSVVVTVIVLYQYHHDDPDGGMKPKWTRVILLNWCAMFLRMKRPGEKVRPACQHK 360
 QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVTPTDPSGVVCGRMACSPHDEHL 420
 DB 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVTPTDPSGVVCGRMACSPHDEHL 420
 QY 421 LHGGQPPEGDPDLAKILEEVRYIANFRFCQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
 DB 421 LHGGQPPEGDPDLAKILEEVRYIANFRFCQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480

QY 481 ICTIGILMSAPNFVEAVSKDFA 502
DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 3
AAB24088
ID AAB24088 standard; protein; 502 AA.
XX AAB24088;
AC AAB24088;

XX 29-JAN-2001 (first entry)
XX Human PRO2145 protein sequence SEQ ID NO:77.

XX Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
KW proliferation; tumorigenesis; identification; cancer; cytostatic;
KW neurotropic; neuroprotective; antiinflammatory; immunosuppressive;
KW immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;
KW neuronal disorder; glial disorder; astrocytal disorder; angiogenic;
KW hypothalamic disorder; glandular disorder; macrophagal disorder;
KW epithelial disorder; stromal disorder; blastocoelec disorder;
KW inflammatory disorder; immunologic disorder.

XX Homo sapiens.

OS WO200053755-A2.

PN 14-SEP-2000.

PD 06-JAN-2000; 2000WO-US000376.

XX 08-MAR-1999; 99WO-US005028.

PR 02-JUN-1999; 99WO-US012252.

PR 23-JUN-1999; 99US-0141037P.

PR 07-JUL-1999; 99US-0143048P.

PR 26-JUL-1999; 99US-0145698P.

PR 30-NOV-1999; 99WO-US028313.

PR 20-DEC-1999; 99WO-US030911.

PR 05-JAN-2000; 2000WO-US000219.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hallan KJ, Roy MA;
PI Watanabe CK, Wood WI;
PI WPI; 2000-572270/53.
XX N-PSDB; AAC58395.

XX Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
XX treatment, diagnosis and prevention of cancer.

XX Claim 61; Fig 58; 286pp; English.

XX The present invention describes an isolated antibody that binds to one of
XX the human PRO proteins designated PRO212, PRO290, PRO341, PRO535, PRO619,
XX PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009, PRO1025,
XX PRO1030, PRO1097, PRO1107, PRO1153, PRO1182, PRO1184, PRO1187,
XX PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094, PRO2145 OR
XX PRO2198. PRO antagonists can be used to inhibit tumour cell growth. The
XX PRO polypeptides and nucleotides are useful in the treatment, diagnosis
XX and prevention of cancer. The antibodies and other anti-tumour compounds
XX maybe used to treat various conditions, including those characterised by
XX overexpression and/or activation of the amplified PRO genes. Exemplary
XX conditions or disorders to be treated with such antibodies and other
XX compounds include benign or malignant tumours (e.g., renal, liver,
XX kidney, bladder, breast, gastric, ovarian, colorectal, prostate,
XX pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas,
XX glioblastomas, and various head and neck tumours), leukaemias and
XX lymphoid malignancies, other disorders such as neuronal, glial,
XX astrocytal, hypothalamic and other glandular, macrophagal, epithelial,
XX stromal and blastocoelec disorders, and inflammatory, angiogenic and
XX immunologic disorders. AAC58242 to AAC58366 represent PCR primers and

CC hybridisation probes used in the isolation of the human PRO sequences.
CC AAC58367 to AAC58396 and AAC24057 to AAC24089 represent human PRO
CC polynucleotide and protein sequences given in the exemplification of the
CC present invention
XX Sequence 502 AA;
SQ

Query Match 100.0%; Score 2702; DB 3; Length 502;
Best Local Similarity 100.0%; Pred. No. 6.9e-264;
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAASLLHVSLLQGEFQKLYKELVKNYNPLERPVANDSOPLTVYLSLL 60
DB 1 MRCSPGGVWLAASLLHVSLLQGEFQKLYKELVKNYNPLERPVANDSOPLTVYLSLL 60
QY 61 QTMVDENKQVLTNTIMLQMSWTDLHVNSEYFGVKTVPFDDGIWKPDILLYNSADE 120
DB 61 QTMVDENKQVLTNTIMLQMSWTDLHVNSEYFGVKTVPFDDGIWKPDILLYNSADE 120
QY 121 RFDAFTHTNVLVNSGHCQYLPPIGFKSSCYIDVRFDDVQVCKLKFGSWYGGWSL 180
DB 121 RFDAFTHTNVLVNSGHCQYLPPIGFKSSCYIDVRFDDVQVCKLKFGSWYGGWSL 180
QY 181 QMOEADISGVIENGWDLVGIPKRSERFECKEYPDVTFTVMRRRTLYVGLNLLIP 240
DB 181 QMOEADISGVIENGWDLVGIPKRSERFECKEYPDVTFTVMRRRTLYVGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTVFMLVAEIMPATSDSVPLIAQYFAST 300
DB 241 CVLISALALLVFLPADSGEKISLGITVLLSLTVFMLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIVGLSVVTVIVLYQHHDDPGGKMPKWTTRVILLNWCAPLEMKERGEDKVRPACQHK 360
DB 301 MIIVGLSVVTVIVLYQHHDDPGGKMPKWTTRVILLNWCAPLEMKERGEDKVRPACQHK 360
QY 361 QRCESLASVEMSAVAPPASNGNLLYIGRGLDGVCVTPDPSGVVCGMACSPTHDEHL 420
DB 361 QRCESLASVEMSAVAPPASNGNLLYIGRGLDGVCVTPDPSGVVCGMACSPTHDEHL 420
QY 421 LHGGQPPGDPDLAKILEEVRYIANFRQDSEAVCSWKFAACVVDRLCLMAFSVFTI 480
DB 421 LHGGQPPGDPDLAKILEEVRYIANFRQDSEAVCSWKFAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 4
AAB2690
ID AAB2690 standard; protein; 502 AA.
XX AAB2690;
XX 15-OCT-2001 (first entry)
DT Nicotinic acetylcholine receptor alpha7.
XX Nicotinic acetylcholine receptor; nAChR; human;
KW acetylcholine binding protein; AChBP; mollusc; ligand-binding protein;
KW ligand-gated ion channel; crystal; drug design; protein co-ordinate data;
KW schizophrenia; Alzheimer's disease; nicotine addiction;
KW Tourette's syndrome; therapy; neurotropic; neuroprotective.
XX Homo sapiens.
XX Key Location/Qualifiers
PH 108..115
FT /note= "conserved ligand-binding region, residues Trp108
FT and Tyr115 are essential"
FT 171..173
FT /note= "conserved ligand-binding region, residues Trp171
FT and Tyr173 are essential"
FT

Region 210..217
/note= "conserved ligand-binding region, residues Tyr210,
Cys212, Cys213 and Tyr217 are essential"

WO200158951-A2.
16-AUG-2001.
09-FEB-2001; 2001WO-EP001457.
10-FEB-2000; 2000EP-00200443.
31-OCT-2000; 2000EP-00203810.
(TEWE-) STICHTING TECH WETENSCHAPPEN.

PI Smit AB, Sixma TK;
WPI; 2001-497071/54.

Water-soluble ligand-binding proteins derived from molluscs and analogs of ligand-gated ion channels, useful in drug screening assay, where the drugs identified can be used in the treatment of Alzheimer's disease or schizophrenia.

Disclosure: Page 252-254; 260pp; English.

The present sequence is that of the alpha subunit of human nicotinic acetylcholine receptor (nAChR). The sequence includes regions that are conserved throughout the various nAChR alpha subunits and which are essential for ligand binding. The invention relates to water-soluble ligand-binding proteins derived from molluscs, especially acetylcholine-binding proteins (AChBPs) and analogues of ligand-gated ion channels, their crystals, and their use for screening ligands of ligand-gated ion channels. The water-soluble ligand-binding proteins are capable of forming multimers and are amenable to crystallization. The crystal structure of AChBP is provided, and can be used to generate 3D models of the extracellular ligand-binding domain of ligand-gated ion channels and thus for screening of drugs that act on these ion channels. Chimeric proteins are provided that are capable of binding a ligand of a ligand-gated receptor, and comprise at least the amino acids of the AChBP determining solubility of the AChBP, in the same positions as in the AChBP, and also comprising amino acids determining binding to the ligand. In the chimeric proteins, at least the essential amino acids of at least 1 of the conserved regions of an nAChR have been substituted for the corresponding amino acids, and preferably entire stretches have been substituted. New drugs can be developed that selectively intervene in neuronal signalling pathways, especially where the ligand-gated ion channel is the nAChR, and the related disorder is Tourette's syndrome, Alzheimer's disease, addiction to nicotine or schizophrenia.

XX Sequence 502 AA;

Query Match 100.0%; Score 2702; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 6.9e-264;
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRCSPGVWMLAASLLHVSLSQGEFORKLYKELVKYNPLERPVANDSQPLTVYFSLSL 60
DB 1 MRCSPGVWMLAASLLHVSLSQGEFORKLYKELVKYNPLERPVANDSQPLTVYFSLSL 60

QY 61 QIMDVDEKNOVLTNIWQMSWTDHYLQWNVSEYPGVKTVRFPDQGIWKPDILLYNSADE 120
DB 61 QIMDVDEKNOVLTNIWQMSWTDHYLQWNVSEYPGVKTVRFPDQGIWKPDILLYNSADE 120

QY 121 RFDAFTFTNVLNNSGHCQYLPGIFKSSCVIDVRWPFDDVQCKLKFGSWSGWSL 180
DB 121 RFDAFTFTNVLNNSGHCQYLPGIFKSSCVIDVRWPFDDVQCKLKFGSWSGWSL 180

QY 181 QM0EADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTVFTVMRRRTLYYGLNLLIP 240
DB 181 QM0EADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTVFTVMRRRTLYYGLNLLIP 240

QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFAST 300

DB 241 CVLISALALLVFLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFAST 300

QY 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTTRVILLNWCWFLMKRPGEDKVPACQHK 360

DB 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTTRVILLNWCWFLMKRPGEDKVPACQHK 360

QY 361 QRCCLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTDSDGVVCGMACSPTHDEHL 420

DB 361 QRCCLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTDSDGVVCGMACSPTHDEHL 420

QY 421 LHGGQPPGPDLLAKILIEVRYIANRRCODESAVCSWKFAACVVDRCLCLMAFSVFTI 480

DB 421 LHGGQPPGPDLLAKILIEVRYIANRRCODESAVCSWKFAACVVDRCLCLMAFSVFTI 480

QY 481 ICTIGILMSAPNFVEAVSKDPA 502

DB 481 ICTIGILMSAPNFVEAVSKDPA 502

RESULT 5
AAB50012
ID AAB50012 standard; protein; 502 AA.
XX AC AAB50012;
XX DT 14-MAR-2001 (first entry)
XX DE Wild-type human alpha7 ligand gated ion channel.
XX KW Human; alpha7 nicotinic acetylcholine gated ion channel;
XX KW 5-hydroxytryptamine; 5-HT3; calcium ion conductance.
XX OS Homo sapiens.
XX PN WO200073431-A2.
XX PD 07-DEC-2000.
XX PF 25-MAY-2000; 2000WO-US011862.
XX PR 27-MAY-1999; 99US-0136174P.
XX PA (PHAA) PHARMACIA & UPJOHN CO.
XX PI Groppi VE, Wolfe ML, Berkenpas MB;
XX DR WPI; 2001-061524/07.
XX DR N-PSDB; AAC90380.
XX PT Special cell culture medium for treating cells and for inducing mammalian cell lines to conduct calcium ions, comprising specified concentrations of ions of sodium, calcium and potassium at specified pH.
XX PS Disclosure; Page 61-63; 77pp; English.
XX CC The present sequence is wild-type human alpha7 nicotinic acetylcholine gated ion channel. The human alpha7 ion channel was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells in the present invention, resulting in preferential calcium ion conductance by the cells

XX Sequence 502 AA;

Query Match 100.0%; Score 2702; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 6.9e-264;
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRCSPGVWMLAASLLHVSLSQGEFORKLYKELVKYNPLERPVANDSQPLTVYFSLSL 60
DB 1 MRCSPGVWMLAASLLHVSLSQGEFORKLYKELVKYNPLERPVANDSQPLTVYFSLSL 60

PF	29-OCT-2001; 2001WO-US050985.	RESULT 8	
XX		ADAL0874	
PR	01-NOV-2000; 2000US-00703951.	ID	ADAL0874 standard; protein; 502 AA.
XX		AC	ADAL0874;
PA	(MERI) MERCK & CO INC.	XX	
PI	Gillespie A, Claeps BO, Chavez-Noriega LE, Siegel R, Elliott KJ;	DE	06-NOV-2003 (first entry)
XX		XX	Human neuronal nicotinic acetylcholine receptor alpha 7 subunit #1.
XX		DE	alpha 7 subunit; human; neuronal nicotinic acetylcholine receptor;
DR	WPI; 2002-698532/75.	KW	ligand-gated ion channel; synaptic transmission; gene therapy;
DR	N-PSDB; ABV73248.	KW	transgenic; receptor.
XX		XX	Homo sapiens.
XX		XX	US6524789-B1.
XX		XX	25-FEB-2003.
CC	The invention relates to a suitable host cell transfected with an	XX	07-JUN-1996; 96US-00660451.
CC	isolated nucleic acid molecule comprising a sequence of nucleotides or	XX	07-JUN-1995; 95US-00484722.
CC	ribonucleotides that encodes at least one alpha or beta subunit of a	PA	(MERI) MERCK & CO INC.
CC	human neuronal nicotinic acetylcholine receptor (NACHR). The compositions	XX	Elliott KJ, Harpold MM;
CC	and methods of the present invention, which provide a means to prepare	XX	WPI: 2003-511917/48.
CC	synthetic or recombinant receptors and receptor subunits that are	DR	N-PSDB; ADAL0864.
CC	substantially free of contamination from many other receptor proteins,	XX	New nucleic acid encoding an alpha-6 or a beta-3 subunit of a human
CC	are useful for observing the effect of a drug substance on a particular	PT	neuronal nicotinic acetylcholine receptor (NACHR), useful for identifying
CC	subtype to perform in vitro screening of the drug substance in a test	PT	compounds that modulate human neuronal nACHR activity.
CC	system that is specific for humans. The antibodies can be used in	XX	Disclosure; Col 67-72; 63pp; English.
CC	immunohistochemistry and for diagnostic and therapeutic applications. The	XX	The invention relates to an isolated nucleic acid molecule comprising a
CC	present sequence represents a human neuronal NACHR alpha7 subunit	CC	nucleotide sequence encoding an alpha 6 or a beta 3 subunit of a human
XX		CC	neuronal nicotinic acetylcholine receptor NACHR. NACHR's form ligand-
SQ	Sequence 502 AA;	CC	gated ion channels that mediate synaptic transmissions between nerve and
		CC	muscle and between neurons upon interaction with the neurotransmitter
		CC	acetylcholine. The nucleic acid molecule is useful for identifying
		CC	compounds that modulate human neuronal nACHR. The present sequence
		CC	represents the amino acid sequence of the human neuronal nicotinic
		CC	acetylcholine receptor, NACHR, alpha 7 subunit #1. Note: the present
		CC	sequence is the sequence encoded by the NACHR alpha 7 subunit DNA
		CC	ADAL0864.
		XX	Sequence 502 AA;
		SQ	
			Query Match 100.0%; Score 2702; DB 7; Length 502;
			Best Local Similarity 100.0%; Pred. No. 6.9e-264;
			Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MRCSPGGWMLAALSHVSLQGEFQKLYKELVKNYNPLRPVANDSPLTVYFSLSL 60	QY	1 MRCSPGGWMLAALSHVSLQGEFQKLYKELVKNYNPLRPVANDSPLTVYFSLSL 60
Db	1 MRCSPGGWMLAALSHVSLQGEFQKLYKELVKNYNPLRPVANDSPLTVYFSLSL 60	Db	1 MRCSPGGWMLAALSHVSLQGEFQKLYKELVKNYNPLRPVANDSPLTVYFSLSL 60
QY	61 QIMDVEKQVLTNTNWLQMSWDHYLQWNVSEYPGVKTVPDQIWKPDILLYNSADE 120	QY	61 QIMDVEKQVLTNTNWLQMSWDHYLQWNVSEYPGVKTVPDQIWKPDILLYNSADE 120
Db	61 QIMDVEKQVLTNTNWLQMSWDHYLQWNVSEYPGVKTVPDQIWKPDILLYNSADE 120	Db	61 QIMDVEKQVLTNTNWLQMSWDHYLQWNVSEYPGVKTVPDQIWKPDILLYNSADE 120
QY	121 RFDATHTNVLNNSGHCQYLPGIFKSSCYIDVRWPFDDVQHKLFKFSWSYGGSLDL 180	QY	121 RFDATHTNVLNNSGHCQYLPGIFKSSCYIDVRWPFDDVQHKLFKFSWSYGGSLDL 180
Db	121 RFDATHTNVLNNSGHCQYLPGIFKSSCYIDVRWPFDDVQHKLFKFSWSYGGSLDL 180	Db	121 RFDATHTNVLNNSGHCQYLPGIFKSSCYIDVRWPFDDVQHKLFKFSWSYGGSLDL 180
QY	181 QMQEADISGYIPNGEWDLVGIPKRSRFRFYECCKEYPDVTFTVWRRRTLYYGLNLLIP 240	QY	181 QMQEADISGYIPNGEWDLVGIPKRSRFRFYECCKEYPDVTFTVWRRRTLYYGLNLLIP 240
Db	181 QMQEADISGYIPNGEWDLVGIPKRSRFRFYECCKEYPDVTFTVWRRRTLYYGLNLLIP 240	Db	181 QMQEADISGYIPNGEWDLVGIPKRSRFRFYECCKEYPDVTFTVWRRRTLYYGLNLLIP 240
QY	481 ICTIGILMSAPNFVEAVSKDFA 502	QY	481 ICTIGILMSAPNFVEAVSKDFA 502
Db	481 ICTIGILMSAPNFVEAVSKDFA 502	Db	481 ICTIGILMSAPNFVEAVSKDFA 502

Db 241 CVLISALALLVLLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQVFAST 300
Qy 301 MIIVGLSVVTVTVLQYHHDDPGGKMPKWTAVILLNWCANFLMKRPGEDKVRPACQHK 360
Db 301 MIIVGLSVVTVTVLQYHHDDPGGKMPKWTAVILLNWCANFLMKRPGEDKVRPACQHK 360
Qy 361 QRCRSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVTPDPSGVVCGRMACSPTHDEHL 420
Db 361 QRCRSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVTPDPSGVVCGRMACSPTHDEHL 420
Qy 421 LHGGQPPEGDPDLAKILEEVRYIANFRCDSEAVCSEWKFACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPEGDPDLAKILEEVRYIANFRCDSEAVCSEWKFACVVDRLCLMAFSVFTI 480
Qy 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 9
ID ADD47051 standard; protein; 502 AA.
XX ADD47051;
AC ADD47051;
XX 29-JAN-2004 (first entry)
XX Human Protein NP_000737, SEQ ID NO 12739.
DE Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX Homo sapiens.
XX WO2003016475-A2.
XX 27-FEB-2003.
XX 14-AUG-2002; 2002WO-US025765.
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX (GEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
XX GENBANK; NP_000737.
XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a
XX compound that regulates the activity of one or more of the
XX polynucleotides, a method for producing a pharmaceutical composition, a
XX method for identifying a compound or small molecule that regulates the

CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIFO at
CC ftp.wifo.int/pub/published_pct_sequences.
XX Sequence 502 AA;
SQ
Query Match 100.0%; Score 2702; DB 7; Length 502;
Best Local Similarity 100.0%; Pred. No. 6.9e-264;
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MRCSPGGVWLAAALHVSLSQGEFQKLYKELVKNYNPLERPVANDSPLTVYFSLSL 60
Db 1 MRCSPGGVWLAAALHVSLSQGEFQKLYKELVKNYNPLERPVANDSPLTVYFSLSL 60
Qy 61 QIMDVDEKQVLTNTNWLQMSWTDHYLQWNVSEYPGVKTVPDGOIWKPDILLYNSADE 120
Db 61 QIMDVDEKQVLTNTNWLQMSWTDHYLQWNVSEYPGVKTVPDGOIWKPDILLYNSADE 120
Qy 121 RFDATFHTNVLVNSSGCHCOYLPPIKSCYIDVRWFPDVOHCKLKFGSWSYGGWSLDL 180
Db 121 RFDATFHTNVLVNSSGCHCOYLPPIKSCYIDVRWFPDVOHCKLKFGSWSYGGWSLDL 180
Qy 181 QMQEADISGYIPNGEWDLVGIFPKRSERFEYCKEYPDVTFTVTRRTLYYGLNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGIFPKRSERFEYCKEYPDVTFTVTRRTLYYGLNLLIP 240
Qy 241 CVLISALALLVLLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQVFAST 300
Db 241 CVLISALALLVLLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQVFAST 300
Qy 301 MIIVGLSVVTVTVLQYHHDDPGGKMPKWTAVILLNWCANFLMKRPGEDKVRPACQHK 360
Db 301 MIIVGLSVVTVTVLQYHHDDPGGKMPKWTAVILLNWCANFLMKRPGEDKVRPACQHK 360
Qy 361 QRCRSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVTPDPSGVVCGRMACSPTHDEHL 420
Db 361 QRCRSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVTPDPSGVVCGRMACSPTHDEHL 420
Qy 421 LHGGQPPEGDPDLAKILEEVRYIANFRCDSEAVCSEWKFACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPEGDPDLAKILEEVRYIANFRCDSEAVCSEWKFACVVDRLCLMAFSVFTI 480
Qy 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502
RESULT 10
ADE57310
ID ADE57310 standard; protein; 502 AA.
XX ADE57310;
XX 29-JAN-2004 (first entry)
XX Human Protein P36544, SEQ ID NO 3171.
XX Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX Homo sapiens.
XX WO2003016475-A2.
PN

XX PD 27-FEB-2003.
XX PF 14-AUG-2002; 2002WO-US025765.
XX PR 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX PA (GHO) GEN HOSPITAL CORP.
XX PA (FAR) BAYER AG.
XX PI Woolf C, D'urso D, Befort K, Costigan M;
XX DR WPI; 2003-268312/26.
XX DR GENBANK; P36544.
XX PT New composition comprising two or more isolated polypeptides, useful for
XX PT preparing a medicament for treating pain in an animal.
XX PS Claim 1; Page; 1017pp; English.
XX CC The invention discloses a composition comprising two or more isolated rat
XX CC or human polynucleotides or a polynucleotide which represents a fragment,
XX CC derivative or allelic variation of the nucleic acid sequence. Also
XX CC claimed are a vector comprising the novel polynucleotide, a host cell
XX CC comprising the vector, a method for identifying a nucleotide sequence
XX CC which is differentially regulated in an animal subjected to pain and a
XX CC kit to perform the method, an array, a method for identifying an agent
XX CC that increases or decreases the expression of the polynucleotide sequence
XX CC that is differentially expressed in neuronal tissue of a first animal
XX CC subjected to pain, a method for identifying a compound which regulates
XX CC the expression of a polynucleotide sequence which is differentially
XX CC expressed in an animal subjected to pain, a method for identifying a
XX CC compound that regulates the activity of one or more of the
XX CC polynucleotides, a method for producing a pharmaceutical composition, a
XX CC method for identifying a compound or small molecule that regulates the
XX CC activity in an animal of one or more of the polypeptides given in the
XX CC specification, a method for identifying a compound useful in treating
XX CC pain and a pharmaceutical composition comprising the one or more
XX CC polypeptides or their antibodies. The polynucleotide or the compound that
XX CC modulates its activity is useful for preparing a medicament for treating
XX CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
XX CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
XX CC therapy). The sequence presented is a human protein (shown in Table 2 of
XX CC the specification) which is differentially expressed during pain. Note:
XX CC The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic form directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 502 AA;
Query Match 100.0%; Score 2702; DB 7; Length 502;
Best Local Similarity 100.0%; Pred No. 6.9e-264;
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRCSPGGVWLAAASLLHVSQGEFQKLYKELVKNVPLERPVANDSQPLTVFSLSL 60
Db 1 MRCSPGGVWLAAASLLHVSQGEFQKLYKELVKNVPLERPVANDSQPLTVFSLSL 60
QY 61 QIMDVDEKQVLTNTLWQMSWDHVLQNVSEYPGVKTVPDGOIKWPDILLYNSADE 120
Db 61 QIMDVDEKQVLTNTLWQMSWDHVLQNVSEYPGVKTVPDGOIKWPDILLYNSADE 120
QY 121 RFDATHTNVLNNSGHCQVLPFGIKSSCYIDVRWFFPDVQCKLKFGSWSYCGMSLDL 180
Db 121 RFDATHTNVLNNSGHCQVLPFGIKSSCYIDVRWFFPDVQCKLKFGSWSYCGMSLDL 180
QY 181 QMQEADISGYIPNGEWDLVGPKGRSERFYECCKEYPDVTFTVWRRRTLYYGLNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGPKGRSERFYECCKEYPDVTFTVWRRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTVFLLVAEIMPATSDSVPLIAQYFAST 300

Db 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTVFLLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIIVGLSVVTVIIVLOYHHDPDGGKMPKWTREVILLNWCAMFLMKRPGEDKVRPACQHK 360
Db 301 MIIIVGLSVVTVIIVLOYHHDPDGGKMPKWTREVILLNWCAMFLMKRPGEDKVRPACQHK 360
QY 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTDPDSGVVCGMACSPTHDEHL 420
Db 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTDPDSGVVCGMACSPTHDEHL 420
QY 421 LHGGOPPEGDDLAKILEEVYIANRFRQDESEAVCSEWKFAPACVDRCLCMASFVFTI 480
Db 421 LHGGOPPEGDDLAKILEEVYIANRFRQDESEAVCSEWKFAPACVDRCLCMASFVFTI 480
QY 481 ICTIGILMSAFNFVEAVSKDFA 502
Db 481 ICTIGILMSAFNFVEAVSKDFA 502
RESULT 11
AAW69216
ID AAW69216 standard; protein; 502 AA.
XX AC
XX AA W69216;
XX DT 09-OCT-1998 (first entry)
XX DE V274T variant human alpha7 nAChR protein.
XX KW Alpha7 nAChR; alpha7 nicotinic acetylcholine receptor subunit; cancer;
XX KW neurodegeneration; enzyme dysfunction; affective disorder; therapy;
XX KW immune dysfunction; diabetic neuropathy; Alzheimer's disease;
XX KW schizophrenia.
XX OS Homo sapiens.
XX PN WO9828331-A2.
XX PD 02-JUL-1998.
XX PF 22-DEC-1997; 97WO-US023405.
XX PR 20-DEC-1996; 96US-00771737.
XX PA (ABBO) ABBOTT LAB.
XX PI Briggs CA, Gopalakrishnan M, McKenna DG, Monteggia LM, Roch J;
XX PI Sullivan JP, Touma E;
XX DR WPI; 1998-377593/32.
XX DR N-PSDB; AAV44687.
XX PT Nucleic acid encoding variant of human alpha 7 nicotinic acetylcholine
XX PT receptor sub-unit - used to identify modulators of the receptor,
XX PT potentially useful for treating neuro-degeneration, cancer etc.
XX PS Claim 15; Fig 2; 44pp; English.
XX CC This sequence is the V247T variant of human alpha7 nicotinic
XX CC acetylcholine receptor (nAChR) subunit of the invention. Cells containing
XX CC the DNA are used to express the protein and to identify modulators of
XX CC alpha7 nAChR activity or cytoprotective agents, e.g. antisense compounds
XX CC or antagonists that are potentially useful for treating
XX CC neurodegeneration, enzyme dysfunction, affective disorders and immune
XX CC dysfunction, such as cancer, post-herpetic neuralgia, diabetic
XX CC neuropathy, osteoarthritis, Alzheimer's or Parkinson's diseases, kuru,
XX CC psychosis and schizophrenia. Probes based on the DNA are used to detect
XX CC the DNA in usual hybridisation or amplification tests, while monoclonal
XX CC antibodies are used to detect the protein for diagnosis (in vitro or by
XX CC in situ immuno-fluorescent assay). Compared with wild-type alpha7 nAChR,
XX CC the protein has about 100-fold greater sensitivity to cholinergic
XX CC receptor agonists (nicotine or acetylcholine) and response to these

CC agonists decays more slowly, but the wild-type inward rectification is retained

XX Sequence 502 AA;

Query Match 99.9%; Score 2698; DB 2; Length 502;
 Best Local Similarity 99.8%; Pred. No. 1.7e-263;
 Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGGWMLAASLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSL 60
 DB 1 MRCSPGGWMLAASLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSL 60

QY 61 QIMDVDEKNQVLTNIWQMSWTDHYLQWNVSEYPGVKTFRPDGQIWKPDILLYNSADE 120
 DB 61 QIMDVDEKNQVLTNIWQMSWTDHYLQWNVSEYPGVKTFRPDGQIWKPDILLYNSADE 120

QY 121 RFDATFTNVLNVSNGHCQVLPFGIFKSSCYIDVRWFFDVQHCKLFGWSYCGWSLDL 180
 DB 121 RFDATFTNVLNVSNGHCQVLPFGIFKSSCYIDVRWFFDVQHCKLFGWSYCGWSLDL 180

QY 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFVTMRRRTLYYGLNLLIP 240
 DB 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFVTMRRRTLYYGLNLLIP 240

QY 241 CVLISALALLVFLIPADSGEKISLGIITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFAS 300
 DB 241 CVLISALALLVFLIPADSGEKISLGIITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFAS 300

QY 301 MIIVGLSVVTVIVLYQHHDPPDGKMPKTRVILLNWCAMFLMRKRPGEKVRPACQHK 360
 DB 301 MIIVGLSVVTVIVLYQHHDPPDGKMPKTRVILLNWCAMFLMRKRPGEKVRPACQHK 360

QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCYPTPDGSGVCGMACSPTHDEHL 420
 DB 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCYPTPDGSGVCGMACSPTHDEHL 420

QY 421 LHGGOPPEGDPDLAKILEEVRYIANRFRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
 DB 421 LHGGOPPEGDPDLAKILEEVRYIANRFRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480

QY 481 ICTGILMSAPNFVEAVSKDFA 502
 DB 481 ICTGILMSAPNFVEAVSKDFA 502

RESULT 12
 AAB50015 standard; protein; 502 AA.
 AAB50015;
 AAB50015;
 14-MAR-2001 (first entry)
 Mutant human alpha7 ligand gated ion channel #1.
 Human; alpha7 nicotinic acetylcholine gated ion channel; mutant;
 5-hydroxytryptamine; 5-HT3; calcium ion conductance; mutein.
 Homo sapiens.
 OS Synthetic.
 Key Location/Qualifiers
 FT Misc-difference 230 /note= "Wild-type Thr substituted by Pro"
 XX WO200073431-A2.
 XX 07-DEC-2000.
 XX 25-MAY-2000; 2000WO-US011862.
 XX 27-MAY-1999; 99US-0136174P.

XX (PHAA) PHARMACIA & UPJOHN CO.
 XX Groppi VB, Wolfe ML, Berkenpas MB;
 XX WPI; 2001-061524/07.
 XX N-PSDB; AAC90385.
 XX Special cell culture medium for treating cells and for inducing mammalian
 XX cell lines to conduct calcium ions, comprising specified concentrations
 XX of ions of sodium, calcium and potassium at specified pH.
 XX Claim 100; Page 70-72; 77pp; English.
 XX The present sequence is a mutant human alpha7 nicotinic acetylcholine
 XX gated ion channel. The human alpha7 ion channel was used in the
 XX construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand
 XX gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric
 XX ion channel can be expressed by recombinant cells in the present
 XX invention, resulting in preferential calcium ion conductance by the cells
 XX Sequence 502 AA;

Query Match 99.8%; Score 2696; DB 4; Length 502;
 Best Local Similarity 99.8%; Pred. No. 2.8e-263;
 Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGGWMLAASLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSL 60
 DB 1 MRCSPGGWMLAASLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSL 60

QY 61 QIMDVDEKNQVLTNIWQMSWTDHYLQWNVSEYPGVKTFRPDGQIWKPDILLYNSADE 120
 DB 61 QIMDVDEKNQVLTNIWQMSWTDHYLQWNVSEYPGVKTFRPDGQIWKPDILLYNSADE 120

QY 121 RFDATFTNVLNVSNGHCQVLPFGIFKSSCYIDVRWFFDVQHCKLFGWSYCGWSLDL 180
 DB 121 RFDATFTNVLNVSNGHCQVLPFGIFKSSCYIDVRWFFDVQHCKLFGWSYCGWSLDL 180

QY 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFVTMRRRTLYYGLNLLIP 240
 DB 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFVTMRRRTLYYGLNLLIP 240

QY 241 CVLISALALLVFLIPADSGEKISLGIITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFAS 300
 DB 241 CVLISALALLVFLIPADSGEKISLGIITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFAS 300

QY 301 MIIVGLSVVTVIVLYQHHDPPDGKMPKTRVILLNWCAMFLMRKRPGEKVRPACQHK 360
 DB 301 MIIVGLSVVTVIVLYQHHDPPDGKMPKTRVILLNWCAMFLMRKRPGEKVRPACQHK 360

QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCYPTPDGSGVCGMACSPTHDEHL 420
 DB 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCYPTPDGSGVCGMACSPTHDEHL 420

QY 421 LHGGOPPEGDPDLAKILEEVRYIANRFRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
 DB 421 LHGGOPPEGDPDLAKILEEVRYIANRFRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480

QY 481 ICTGILMSAPNFVEAVSKDFA 502
 DB 481 ICTGILMSAPNFVEAVSKDFA 502

RESULT 13
 AAB50016 standard; protein; 502 AA.
 XX AAB50016;
 XX AAB50016;
 XX 14-MAR-2001 (first entry)
 XX Mutant human alpha7 ligand gated ion channel #2.

XX
KW Human; alpha7 nicotinic acetylcholine gated ion channel; mutant;
KW 5-hydroxytryptamine; 5-HT3; calcium ion conductance; mutein.
XX
OS Homo sapiens.
OS Synthetic.
FH Key Location/Qualifiers
FT Misc-difference 241 /note= "Wild-type Cys substituted by Ser"
XX
XX WO200073431-A2.
XX
XX 07-DEC-2000.
XX
XX 25-MAY-2000; 2000WO-US011862.
XX
XX 27-MAY-1999; 99US-0136174P.
XX
XX (PHAA) PHARMACIA & UPJOHN CO.
XX
XX Groppi VE, Wolfe ML, Berkenpas MB;
XX
XX WPI; 2001-061524/07.
XX
XX N-PSDB; AAC90386.
XX
XX Special cell culture medium for treating cells and for inducing mammalian
XX cell lines to conduct calcium ions, comprising specified concentrations
XX of ions of sodium, calcium and potassium at specified pH.
XX
XX Claim 102; Page 72-74; 77pp; English.
XX
XX The present sequence is a mutant human alpha7 nicotinic acetylcholine
XX gated ion channel. The human alpha7 ion channel was used in the
XX construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand
XX gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric
XX ion channel can be expressed by recombinant cells in the present
XX invention, resulting in preferential calcium ion conductance by the cells
XX
XX Sequence 502 AA;
SQ

Query Match 99.6%; Score 2692; DB 4; Length 502;
Best Local Similarity 99.8%; Pred. No. 7.1e-263;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSGGVWLAAALSHVSLQGEFQKLYKELVKYNPLERPVANDSPLTVYFSLSL 60
Db 1 MRCSGGVWLAAALSHVSLQGEFQKLYKELVKYNPLERPVANDSPLTVYFSLSL 60

QY 61 QIMDVEKQVLTNTNWLQMSWTDHYLQMNVSYPGVKTVRFPDGGQIWKPDILLYNSADE 120
Db 61 QIMDVEKQVLTNTNWLQMSWTDHYLQMNVSYPGVKTVRFPDGGQIWKPDILLYNSADE 120

QY 121 RPDATHNTNVLNNSGHCQVLPDGI FKSSCYIDVRWFPDQVCKLKFGSWSGGWSLDL 180
Db 121 RPDATHNTNVLNNSGHCQVLPDGI FKSSCYIDVRWFPDQVCKLKFGSWSGGWSLDL 180

QY 181 QMOEADISGYPNGEWDLVGIPGKRSEFEYCKEPEYDVTFTVTRRRRLYYGLNLLIP 240
Db 181 QMOEADISGYPNGEWDLVGIPGKRSEFEYCKEPEYDVTFTVTRRRRLYYGLNLLIP 240

QY 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTVFLLVAEIMPATSDSVPFLIAQYFAS 300
Db 241 SVLISALALLVFLPADSGEKISLIGITVLLSLTVFLLVAEIMPATSDSVPFLIAQYFAS 300

QY 301 MIIIVGLSVTVTVIYQHHDDPGCKMPKWTFRVILLNWCANFLBMPKPGEDKVRPACQHK 360
Db 301 MIIIVGLSVTVTVIYQHHDDPGCKMPKWTFRVILLNWCANFLBMPKPGEDKVRPACQHK 360

QY 361 QRRCSLASVMSAVAPPPASNGNLLYIGFRLGDCVHCVPDPDSGVCGMACSPTHDEHL 420
Db 361 QRRCSLASVMSAVAPPPASNGNLLYIGFRLGDCVHCVPDPDSGVCGMACSPTHDEHL 420

QY 421 LHGGQPPEGDPDLAKILEEVRYIANRFRCDQSEAVCSEWKFACVVDRLCIMAFAVSFTI 480
Db 421 LHGGQPPEGDPDLAKILEEVRYIANRFRCDQSEAVCSEWKFACVVDRLCIMAFAVSFTI 480

QY 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 14
AAB50017
ID AAB50017 standard; protein; 502 AA.
XX
XX AC AAB50017;
XX
XX 14-MAR-2001 (first entry)
XX
XX Mutant human alpha7 ligand gated ion channel #3.
XX
XX Human; alpha7 nicotinic acetylcholine gated ion channel; mutant;
XX 5-hydroxytryptamine; 5-HT3; calcium ion conductance; mutein.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 230 /note= "Wild-type Thr substituted by Pro"
XX FT Misc-difference 241 /note= "Wild-type Cys substituted by Ser"
XX
XX WO200073431-A2.
XX
XX 07-DEC-2000.
XX
XX 25-MAY-2000; 2000WO-US011862.
XX
XX 27-MAY-1999; 99US-0136174P.
XX
XX (PHAA) PHARMACIA & UPJOHN CO.
XX
XX Groppi VE, Wolfe ML, Berkenpas MB;
XX
XX WPI; 2001-061524/07.
XX
XX N-PSDB; AAC90387.
XX
XX Special cell culture medium for treating cells and for inducing mammalian
XX cell lines to conduct calcium ions, comprising specified concentrations
XX of ions of sodium, calcium and potassium at specified pH.
XX
XX Claim 104; Page 75-77; 77pp; English.
XX
XX The present sequence is a mutant human alpha7 nicotinic acetylcholine
XX gated ion channel. The human alpha7 ion channel was used in the
XX construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand
XX gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric
XX ion channel can be expressed by recombinant cells in the present
XX invention, resulting in preferential calcium ion conductance by the cells
XX
XX Sequence 502 AA;
SQ

Query Match 99.4%; Score 2686; DB 4; Length 502;
Best Local Similarity 99.6%; Pred. No. 2.9e-262;
Matches 500; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRCSGGVWLAAALSHVSLQGEFQKLYKELVKYNPLERPVANDSPLTVYFSLSL 60
Db 1 MRCSGGVWLAAALSHVSLQGEFQKLYKELVKYNPLERPVANDSPLTVYFSLSL 60

QY 61 QIMDVEKQVLTNTNWLQMSWTDHYLQMNVSYPGVKTVRFPDGGQIWKPDILLYNSADE 120
Db 61 QIMDVEKQVLTNTNWLQMSWTDHYLQMNVSYPGVKTVRFPDGGQIWKPDILLYNSADE 120

121 RFDAFHTNVLNNSGHCQVLPPIGFKSSCYIDVRFPDVOHQCKLKFGSWSYGGWSLDL 180
121 RFDAFHTNVLNNSGHCQVLPPIGFKSSCYIDVRFPDVOHQCKLKFGSWSYGGWSLDL 180
181 QMQEADISGYPNGEWDLVGIPKRSERFYECCKEPYDVTFTVTRRRPLYGLMLLIP 240
181 QMQEADISGYPNGEWDLVGIPKRSERFYECCKEPYDVTFTVTRRRPLYGLMLLIP 240
241 CVLISALALVFLPADSGEKISLIGITVLLSLTFVLLVAEIMPATSDSVPLIAQYFAS 300
241 SVLISALALVFLPADSGEKISLIGITVLLSLTFVLLVAEIMPATSDSVPLIAQYFAS 300
301 MIIIVGLSVVVTIVLQYHHDDPGGKMPKTRVILLNWCAMFLMRKPGDKVRPACQHK 360
301 MIIIVGLSVVVTIVLQYHHDDPGGKMPKTRVILLNWCAMFLMRKPGDKVRPACQHK 360
361 QRCCLASVEMSAVAPPASGNLLYIGFGLDGVHCVPTPDGSGVCGRMACSPTHDEHL 420
361 QRCCLASVEMSAVAPPASGNLLYIGFGLDGVHCVPTPDGSGVCGRMACSPTHDEHL 420
421 LHGGQPEGPDPLAKILLEEVRYIANRFRCODESEAVCSEWKFACVVDRLCLMAFSVFTI 480
421 LHGGQPEGPDPLAKILLEEVRYIANRFRCODESEAVCSEWKFACVVDRLCLMAFSVFTI 480
481 ICTIGILMSAPNFVEAVSKDFA 502
481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 15
ID ADE57308
XX ADE57308 standard; protein; 502 AA.
AC ADE57308;
XX ADE57308;
DT 29-JAN-2004 (first entry)
XX Rat Protein Q05941, SEQ ID NO 3169.
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW Chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX Rattus norvegicus.
XX WO2003016475-A2.
XX 27-FEB-2003.
XX 14-AUG-2002; 2002WO-US025765.
XX 14-AUG-2001; 2001US-0312147P.
XX 01-NOV-2001; 2001US-0346382P.
XX 26-NOV-2001; 2001US-0333347P.
XX (GEHO) GEN HOSPITAL CORP.
XX (FARB) BAYER AG.
XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
XX GENBANK; Q05941.
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat
or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a

CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC the sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 502 AA;

Query Match 93.8%; Score 2535; DB 7; Length 502;
Best Local Similarity 93.6%; Pred. No. 5.4e-247;
Matches 465; Conservative 18; Mismatches 14; Indels 0; Gaps 0;
QY 6 GGVWLAALASLHVLSLQGEFORLYKELVKNYNPLERPVANDSQPLTVYFSLSLQIMDV 65
DB 6 GGIWLAALASLHVLSLQGEFORLYKELVKNYNPLERPVANDSQPLTVYFSLSLQIMDV 65
QY 66 DEKNQVLTINILQMSWTDHYLQNVSEYPGVKTVPDPDQIWKPDILLNSADDERDAT 125
DB 66 DEKNQVLTINILQMSWTDHYLQNVSEYPGVKNVRFPPDQIWKPDILLNSADDERDAT 125
QY 126 FHTNVLNNSGHCQVLPPIGFKSSCYIDVRFPDVOHQCKLKFGSWSYGGWSLDLQMOEA 185
DB 126 FHTNVLNNSGHCQVLPPIGFKSSCYIDVRFPDVOHQCKLKFGSWSYGGWSLDLQMOEA 185
QY 186 DISGYIPNGEWDLVGIPKRSERFYECCKEPYDVTFTVTRRRPLYGLMLLIPCVLIS 245
DB 186 DISGYIPNGEWDLVGIPKRSERFYECCKEPYDVTFTVTRRRPLYGLMLLIPCVLIS 245
QY 246 ALALLVFLPADSGEKISLIGITVLLSLTFVLLVAEIMPATSDSVPLIAQYFAS 305
DB 246 ALALLVFLPADSGEKISLIGITVLLSLTFVLLVAEIMPATSDSVPLIAQYFAS 305
QY 306 LSVVVTIVLQYHHDDPGGKMPKTRVILLNWCAMFLMRKPGDKVRPACQHKRRC 365
DB 306 LSVVVTIVLQYHHDDPGGKMPKTRVILLNWCAMFLMRKPGDKVRPACQHKRRC 365
QY 366 LASVEMSAVAPPASGNLLYIGFGLDGVHCVPTPDGSGVCGRMACSPTHDEHLHGGQ 425
DB 366 LASVEMSAVAPPASGNLLYIGFGLDGVHCVPTPDGSGVCGRMACSPTHDEHLHGGQ 425
QY 426 PPEGDPLAKILLEEVRYIANRFRCODESEAVCSEWKFACVVDRLCLMAFSVFTICTIG 485
DB 426 PPEGDPLAKILLEEVRYIANRFRCODESEAVCSEWKFACVVDRLCLMAFSVFTICTIG 485
QY 486 ILMGAPNFVEAVSKDFA 502
DB 486 ILMGAPNFVEAVSKDFA 502

Search completed: May 5, 2004, 15:30:00
Job time : 62 secs

GenCore version 5.1.6
Copyright: (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 17:59:31 ; Search time 5017 Seconds
(without alignments)

11166.325 Million cell updates/sec

Title: US-09-703-951A-11

Perfect score: 1876

Sequence: 1 GGCGCAGGCGCAGCGCCGG.....TGCTGGAAGCCCTTCGGA 1876

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_estc:*

9: gb_est1:*

10: gb_est2:*

11: gb_estc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	936	49.9	1201	9	AL530299
2	788.4	42.0	1201	9	AL563701
3	784.4	41.8	1034	13	BX386932
4	784	41.8	908	13	BU149265

ALIGNMENTS

RESULT 1

AL530299

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AL530299 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
CDNA clone CS0DD007YP05 5-PRIME, mRNA sequence.

AL530299.2 GI:31068132

EST.

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1201)

Li W.B., Gruber C., Jesses, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 13, 2001 this sequence version replaced gi:12793792.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster

7646.r For more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DD007CH03Q1&cluster=7646.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :

5	698.2	37.2	1034	13	BX403124
6	653.6	34.8	731	12	BG395536
7	653.2	34.8	738	12	BG925223
8	603.4	32.2	615	14	CB149460
9	560.4	29.9	1084	13	BQ894356
10	517.4	27.6	817	12	BM451308
11	506.4	27.0	536	12	BI963064
12	488.4	26.0	954	9	AA706348
13	488.4	26.0	490	13	BG282644
14	488.8	25.9	795	12	BG288825
15	486.8	25.9	1080	13	BQ070018
16	480.8	25.6	784	14	CA325260
17	478.6	25.5	640	14	CB244439
18	458.8	24.5	789	9	AI742004
19	447	23.8	922	13	BU915857
20	443.6	23.6	1125	13	BU148759
21	420.4	22.4	513	9	AA436529
22	376.8	20.1	651	12	BI917899
23	371.6	19.8	443	9	AV727668
24	362.2	19.3	2296	14	CD013901
25	354.4	18.9	530	9	AA612742
26	350.6	18.7	443	14	W31507
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28	332.2	17.7	586	13	BX299163
29	331	17.6	480	10	BF507825
30	329.2	17.5	635	13	BU680930
31	323.4	17.2	502	9	AA622550
32	323	17.2	549	9	AA418899
33	306.8	16.4	560	14	W52861
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35	306.8	16.4	2815	11	AK034208
36	305	16.3	613	13	BU619901
37	294.2	15.7	885	12	BG632919
38	289.4	15.4	2940	11	AK034228
39	289.4	15.4	3230	11	AK083157
40	283.4	15.1	1436	29	AY402873
41	280	14.9	1864	11	AK053497
42	280	14.9	2916	11	AK051730
43	280	14.9	3126	11	AK080415
44	278.6	14.9	1436	29	AY402874
45	276.2	14.7	477	9	AI306136

AL530299 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
CDNA clone CS0DD007YP05 5-PRIME, mRNA sequence.

AL530299.2 GI:31068132

EST.

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1201)

Li W.B., Gruber C., Jesses, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 13, 2001 this sequence version replaced gi:12793792.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster

7646.r For more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DD007CH03Q1&cluster=7646.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :

[illegible]

```

428 GCGGTGTCACAAAGACTTTGCGTAACACGCGCTGTTCTGTACATGTGAAAACTCACAGG 369
1618 TGGGCAAGGCGCTTTGGCTTGGCGAGATTTGGGGGTGCTAAATCCAGGACAGCATTAACAGC 1677
368 TGGGCAAGGCGCTTTGGCTTGGCGAGATTTGGGGGTGCTAAATCCAGGACAGCGTTACAGC 309
1678 CACAACCTCAGTGTTCCTTCTGGCTGTCAAGTGTGCTTGTCTTACCGTTTCTTTGTACTT 1737
308 CACAACCTCAGTGTTCCTTCTGGCTTGTGAGTGTGCTTACCGTTTCTTTGTACTT 249
1738 TAGGTAGTAGAATCTCAGACATTTTTCATATTTCTCAGATGGGCTGATAGATTCCTTTG 1797
248 TAGGTAGTAGAATCTCAGACATTTTTCATATTTCTCAGATGGGCTGATAGATTCCTTTG 189
1798 GCACATCCGTACCATCGGTTCAGCAGGCGCACTGAGTAGTGCATTTTGGCCCATTTAGCCCACT 1857
198 GCACATCCGTACCATCGGTTCAGCAGGCGCACTTGGGAGTCATTTTGGCCCATTTAGCCCACT 129
1858 GCCTGGAAAGCCCT 1871
128 GCCTGGAAAGCCCT 115

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```

RESULT 4
BUI49265
LOCUS
DEFINITION
AGENCOURT 8443358 Lupski sympathetic_trunk Homo sapiens cDNA clone
IMAGE:6192234 5', mRNA sequence.
ACCESSION
BUI49265
VERSION
BUI49265.1 GI:22662797
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
Organism
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 908)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL3593 row: 0 column: 19
High quality sequence stop: 598.

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FEATURES

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source
1..908
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6192234"
/sex="male"
/tissue_type="sympathetic trunk"
/dev_stage="adult, 16 yr"
/lab_host="DH108"
/clone_lib="lupski sympathetic trunk"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site 1:
NotI; Site 2: SalI; cDNA made by oligo-dr priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACCGTCCG-3' and
5'-GACTAGTCTAGATCGGCGCGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.9 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine); available through Life
Technologies."

```

ORIGIN

```

Query Match 41.8%; Score 784; DB 13; Length 908;
Best Local Similarity 96.1%; Pred. No. 6e-144;
Matches 859; Conservative 0; Mismatches 25; Indels 10; Gaps 5;
QY 4 CGCAGGCGCAGCGCGCGGCGACAGCGTGGAGCGCGCGCGCTCGCTGCAGCTCCG 63
DB 1 CGCAGGCGCAGCGCGCGGCGACAGCGGAGCGCGCGCGCTCGCTGCAGCTCCG 60
QY 64 GGAATCAACATGCGCTGCTCGCGGCGGAGCGCTCTGGCTGGCGCGCTCGCTCGCTG 123
DB 61 GGAATCAACATGCGCTGCTCGCGGCGGAGCGCTCTGGCTGGCGCGCTCGCTCGCTG 120
QY 124 CAGCTGTCCTCGAAGCGGAGTTCAGAGGAAGCTTTTCAAGAGAGCTGGTCAAGAACTAC 183
DB 121 CAGCTGTCCTCGAAGCGGAGTTCAGAGGAAGCTTTTCAAGAGAGCTGGTCAAGAACTAC 180
QY 184 AATCCCTTGGAGAGCGCGCGTGGCCAAATGACTCGCAACCACTCACCGTCTACTTCTCCCTG 243
DB 181 AATCCCTTGGAGAGCGCGCGTGGCCAAATGACTCGCAACCACTCACCGTCTACTTCTCCCTG 240
QY 244 AGCCTCTCTGAGATCATGGACGTGATGAGAGAAACCAAGTTTAAACCAACCAATTTGG 303
DB 241 AGCCTCTCTGAGATCATGGACGTGATGAGAGAAACCAAGTTTAAACCAACCAATTTGG 300
QY 304 CTGCAATGCTTGGACAGATCACTATTATTCAGTGGATGTCAGATATATCCAGGGCTG 363
DB 301 CTGCAATGCTTGGACAGATCACTATTATTCAGTGGATGTCAGATATATCCAGGGCTG 360
QY 364 AAGACTGTTCTTCCAGATGGCGAGATTTGGAACCAAGATTTCTTCTCTATAACAGT 423
DB 361 AAGACTGTTCTTCCAGATGGCGAGATTTGGAACCAAGATTTCTTCTCTATAACAGT 420
QY 424 GCTGATGAGCGCTTGGACGCCACATTCACACTAACGTTGGTGGTGAATTTCTTGGGAT 483
DB 421 GCTGATGAGCGCTTGGACGCCACATTCACACTAACGTTGGTGGTGAATTTCTTGGGAT 480
QY 484 TGCCAGTACCTGCGCTCCAGGATATTCAGAGTTCTCTCATCATGATGATGCTGTTT 543
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QY 604 TTGATGTGCAGATCGAGGACGATATCAGTGTCTATATCCCAATGGAGAAATGGGAC 663
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QY 664 CTAGTGGGAATCCCGGCAAGAGGAGTGAAGTTTCTATGAGTGTCTGCAAGAGCGCTTAC 723
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QY 724 CCCGATGTACCTTTCACAGTGACCA-TGCGCGCGAGGAGCTCTACTATATGGCTCAACCT 782
DB 721 CCCGATGTACCTTTCACAGTGACCA-TGCGCGCGAGGAGCTCTACTATATGGCTCAACCT 780
QY 783 GCTGATCCCTG--TGTGCTCATCTCCGCGCTCGCC--TGCTGCTGCTCTGCTTCT 837
DB 781 GCTGATCCCTG--TGTGCTCATCTCCGCGCTCGCC--TGCTGCTGCTCTGCTTCT 840
QY 838 GCAGA--TTCCCGGGAGAGATTTCCCTGGGG--ATAACAGTCTTACTCTCTCT 887
DB 841 GGAGATTTCCCGGGAGAGATTTCCCTGGGG--ATAACAGTCTTACTCTCTCT 894

```

```

RESULT 5
BX403124
LOCUS
DEFINITION
CDNA clone CS0DC004YAL2 5-PRIME, mRNA sequence.
ACCESSION
BX403124
VERSION
BX403124.1 GI:30611171

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```

BX403124 1034 bp mRNA linear EST 13-MAY-2003
BX403124 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
CDNA clone CS0DC004YAL2 5-PRIME, mRNA sequence.
BX403124
BX403124.1 GI:30611171

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KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 1034)
JOURNAL Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
COMMENT Full-length cDNA libraries and normalization
 Unpublished (2001)
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 7646.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS1DC001ZG09QPlcluster=7646.r. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS1DC001ZG09QPl.
FEATURES Location/Qualifiers
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 1..1034
 /organism="Homo sapiens"
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 /clone="CS0DC004YA12"
 /tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
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 sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
 Query Match 37.2%; Score 698.2; DB 13; Length 1034;
 Best Local Similarity 80.7%; Pred. No. 5.2e-127;
 Matches 931; Conservative 14; Mismatches 16; Indels 193; Gaps 4;
 4 CGCAGCGCAGCCGCGGCGAGCCGACGACGCTGGAGCGCGCGCTCGCTCAGCTCG 63
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 64 GAGCTCAACATCGCTGCTCGCGGAGCGCTGCTGCTGCGCTGCGCGCTGCTGCTG 123
 125 GAGCTCAACATCGCTGCTCGCGGAGCGCTGCTGCTGCGCTGCGCGCTGCTGCTG 183
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 303 AGCCTCTCGAGATCATGAGCGTGGATGAGAGCAACCAAGTTTAAACCAACATTTGG 362
 304 CTGCAATGCTTTGGACAGATCACTATTACAGTGGATGTGTACAGATATCCAGGGGTG 363
 363 CTGCAAT-----
 370 CTGCAAT-----
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 371 -----
 424 GCTGATGAGCGCTTTGACGCCCATTCACATTAACGTTGTTGTTGTTTCTTCTGGGCAT 483
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 484 TGGCAGTACCTGCTCCAGGCATATTCAAGAGTTCCTGCTACATCGATGTACGCTGGTTT 543

Db 371 -----GGCATATTCAAGAGTTCTCTGCTACATCGATGTAGCTGGTTT 412
 Qy 544 CCCTTTGATGTCAGCACTGCAAACTGAAGTTTGGGTCCTGGTCTTAAAGGAGGTGGTCC 603
 Db 413 CCCTTTGATGTCAGCACTGCAAACTGAAGTTTGGGTCCTGGTCTTAAAGGAGGTGGTCC 472
 Qy 604 TTGATCTGCAGATGTCAGGAGGAGATATCAGTGGCTATATCCCAATGGAGATGGGAC 663
 Db 473 TTGATCTGCAGATGTCAGGAGGAGATATCAGTGGCTATATCCCAATGGAGATGGGAC 532
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 Db 533 CTAGTGGGATCCCGCGCAAGAGGAGTTCATGAGTGTCTGCAAGAGCCCTAC 592
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 Qy 844 TCCGGGAGAGAGATTTCCTCGGGATACAGTCTTACTCTCTTCTTCTTCTTCTTCTGCTG 903
 Db 713 TCCGGGAGAGAGATTTCCTCGGGATACAGTCTTACTCTCTTCTTCTTCTTCTTCTGCTG 772
 Qy 904 CTCGTGCTGAGATCATGCGCGCAACATCCGATTCGGTACCATGATGAGCCAGTACTTC 963
 Db 773 CTCGTGCTGAGATCATGCGCGCMACATCCGATTCGGTACCATGATGAGCCAGTACTTC 832
 Qy 964 GCCAGCACCATGATCATGCTGGCTCTCTCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1023
 Db 833 GCCAGCMCATGATCATGCTGGCTCTCTCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 892
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 Db 953 TGCTGCGCTGGTTCCTTSCGAATGAAGAGCGCCCGGAGGAGCAAGTGGCGCCGCTGCG 1011
 Qy 1144 CAGCAACAGCAGCG 1157
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 RESULT 6
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 LOCUS 602458136Fl NTH_MGC_16 Homo sapiens cDNA clone IMAGE:4580408 5',
 DEFINITION mRNA sequence.
 ACCESSION BG395536
 VERSION BG395536.1 GI:13288984
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 731)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: LLCW1299 row: h column: 09
 High quality sequence stop: 723.

[illegible]

QY 1550 TCGTGGAGCCGCTGTCGAAGACTTTCGTAACCAAGCCGCTGCTGTACATGTGGAATA 1609
 DB 425 TCGTGGAGCCGCTGTCGAAGACTTTCGTAACCAAGCCGCTGCTGTACATGTGGAATA 484
 QY 1610 CTCACAGATGGGCAAGCCCTTTGGCTTGGCGAGATTGGGGGTGCTTAATCCAGGACAGCA 1669
 DB 485 CTCACAGATGGGCAAGCCCTTTGGCTTGGCGAGATTGGGGGTGCTTAATCCAGGACAGCA 544
 QY 1670 TTACAGCCCAAACTCCAGTGTCCCTTCTGGCTGTCAGTCGTGTGCTTACGTTTCTT 1729
 DB 545 TTACAGCCCAAACTCCAGTGTCCCTTCTGGCTGTCAGTCGTGTGCTTACGTTTCTT 604
 QY 1730 TGTACTTTAGGTAGTATGATCTCAGCACTTCTTTTCAATCTCAGATGGGCTGATAGA 1789
 DB 605 TGTACTTTAGGTAGTATGATCTCAGCACTTCTTTTCAATCTCAGATGGGCTGATAGA 664
 QY 1790 TATCCTTGGCACATCCGTACCATCGTTCAGCAGGGCCACTGATGTCATTTGGCCATT 1849
 DB 665 TATCCTTGGCACATCCGTACCATCGTTCAGCAGGGCCACTGATGTCATTTGGCCATT 724
 QY 1850 AGCCCACTGCTGG 1863
 DB 725 AGCCCACTGCTGG 738

 RESULT 8
 CBI49460
 LOCUS
 DEFINITION K-EST0205995 L15CKK1 Homo sapiens cDNA clone L15CKK1-50-D08 5', mRNA sequence.
 CBI49460
 VERSION CBI49460.1 GI:28132277
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 615)
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
 TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 50 row: D column: 08
 High quality sequence stop: 615.
 Location/Qualifiers
 1..615
 /organism="Homo sapiens"
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 /clone="L15CKK1-50-D08"
 /sex="M"
 /cell_line="CK-K1"
 /lab_host="Top10P"
 /clone_lib="L15CKK1"
 /note="Organ: Liver; Vector: pcNS-D2; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand

converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10P, by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN
 Query Match 32.2%; Score 603.4; DB 14; Length 615;
 Best Local Similarity 99.0%; Pred. No. 2e-108;
 Matches 607; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 419 ACAGTCTCATGAGCGCTTTGAGCGCACATTCACACCTAACCGTGTGGTGAATCTCTCG 478
 DB 3 ATATTCTCATAAACGCTTTGACGCCACATTCACACTAACCGTGTGGTGAATCTCTCG 62
 QY 479 GGCATTGCCAGTACCTGCTCCAGGCATATTCAGAGATTTCCTGCTACATCGATGACGCT 538
 DB 63 GGCATTGCCAGTACCTGCTCCAGGCATATTCAGAGATTTCCTGCTACATCGATGACGCT 122
 QY 539 GGTTCCTCCCTTTGATGTGCAGCACTGCAAACTGAAGTTTGGGTCTCTGGTCTTACGGAGCT 598
 DB 123 GGTTCCTCCCTTTGATGTGCAGCACTGCAAACTGAAGTTTGGGTCTCTGGTCTTACGGAGCT 182
 QY 599 GGTTCCTGGATCTGCAGATGCAGGAGCAGATATCAGTGGCTATATCCCAATGGAGAT 658
 DB 183 GGTTCCTGGATCTGCAGATGCAGGAGCAGATATCAGTGGCTATATCCCAATGGAGAT 242
 QY 659 GGCACCTAGTGGCAATCCCGGCAAGAGGAGTCAAAAGTTTCTATGAGTGTGCAAAAGAGC 718
 DB 243 GGCACCTAGTGGCAATCCCGGCAAGAGGAGTCAAAAGTTTCTATGAGTGTGCAAAAGAGC 302
 QY 719 CCTACCCCGATGTCACTTCAAGTGAACATGCGCGCAGGACGCTTACTATGGCTCTCA 778
 DB 303 CCTACCCCGATGTCACTTCAAGTGAACATGCGCGCAGGACGCTTACTATGGCTCTCA 362
 QY 779 ACCTGCTGATCCCTGTGTGCTCATCTCCGCTCGCCCTGCTGGTGTCTCTCTTCCCTG 838
 DB 363 ACCTGCTGATCCCTGTGTGCTCATCTCCGCTCGCCCTGCTGGTGTCTCTCTTCCCTG 422
 QY 839 CAGATTCCGGGGAGAGATTTCCCTGGGGATAACAGTCTTACTCTCTCTTACCGTCTTCA 898
 DB 423 CAGATTCCGGGGAGAGATTTCCCTGGGGATAACAGTCTTACTCTCTCTTACCGTCTTCA 482
 QY 899 TGCTGCTGCTGGCTGAGATCATGCCCAACATCCGATTCGGTACCAATGATGATGCCAGT 958
 DB 483 TGCTGCTGCTGGCTGAGATCATGCCCAACATCCGATTCGGTACCAATGATGATGCCAGT 542
 QY 959 ACTTGGCCAGCACCATCATCATCTGGGGCTCTCGGTGGTGTGTCACGCTGATGCTGTGC 1018
 DB 543 ACTTGGCCAGCACCATCATCATCTGGGGCTCTCGGTGGTGTGTCACGCTGATGCTGTGC 602
 QY 1019 AGTACCACCAACCA 1031
 DB 603 AGTACCACCAACCA 615

 RESULT 9
 BQ894356
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 DEFINITION AGENCOURT_8725920 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:6338722 5', mRNA sequence.
 BQ894356
 VERSION BQ894356.1 GI:22286370
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1084)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Uncontact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLM2532 row: g column: 11
High quality sequence stop: 482.
Location/Qualifiers
1. .1084
/organism="Homo sapiens"
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/clone="IMAGE:6338722"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 47"
/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

FEATURES

source

ORIGIN

Query Match 29.9%; Score 560.4; DB 13; Length 1084;
Best Local Similarity 98.5%; Pred. No. 7.9e-100;
Matches 597; Conservative 0; Mismatches 6; Indels 3; Gaps 3;
QY 1 GCGCGAGCGCAGCGCGCGGCGACAGCGAGCGGTGGAGCGCGCGCTCGCTCGAGCT 60
Db 3 GCGCGAGCGCAGCGCGCGGCGACAGCGAGCGGTGGAGCGCGCGCTCGCTCGAGCT 62
QY 61 CCGGGACTCAACATGGCTGCTCGCGCGAGGGGCTGCTGGCGCTGGCGCGCTCGCTC 120
Db 63 CCGGGACTCAACATGGCTGCTCGCGCGAGGGGCTGCTGGCGCTGGCGCGCTCGCTC 122
QY 121 CTGCAGCTGTCCTGCAAGCGGAGTTCCAGAGGAAGCTTTTCAAGAGTGTGTCAGAAC 180
Db 123 CTGCAGCTGTCCTGCAAGCGGAGTTCCAGAGGAAGCTTTTCAAGAGTGTGTCAGAAC 182
QY 181 TACAACTCTGGAGGCGCGTGGCGCAATGACTCGCAACCTACCGTCTACTCTCC 240
Db 183 TACAACTCTGGAGAGGCGCGTGGCGCAATGACTCGCAACCTACCGTCTACTCTCC 242
QY 241 CTGAGCTCTCTGAGATCATGGACGTGGATGAGAAGAACCAAGTTTTTAACCAACCAATT 300
Db 243 CTGAGCTCTCTGAGATCATGGACGTGGATGAGAAGAACCAAGTTTTTAACCAACCAATT 302
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Db 303 TGGCTGCAATGCTTGGACAGATCACTATTACAGTGGATGTGTCAGAAATCCAGG 362
QY 361 GTCAAGACTGTTCTGTTTCCAGATGGCCAGATTTGGAACCCAGACATTTCTCTATAAC 420
Db 363 GTGAAGACTGTTCTGTTTCCAGATGGCCAGATTTGGAACCCAGACATTTCTCTATAAC 422
QY 421 AGTGCTGATGAGGCTTTTGACGCCACATTCACACATTAACGTTGTGGTGAATTTCTTGGG 480
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QY 481 CATTTGCAGTACCTGCTCCAGGCATATTCAAGATT-CTGTGATCATCATGATGACGCTG 539
Db 483 CATTTGCAGTACCTGCTCCAGGCATATTCAAGATTTCCTGCTACATCATGATGATCCCTG 542
QY 540 GTTTTCCCTTTGATGTGACGACTGCATA-CTGAAGTTTGGGT-CCTGGTCTTACGGAGGC 597
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QY 598 TGGTCC 603
Db 603 TGGTCC 608
RESULT 10
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LOCUS BM451308
DEFINITION AGENCOURT_6386438 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5493819
5', mRNA sequence.
ACCESSION BM451308
VERSION BM451308.1 GI:18500348
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 817)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLM12118 row: c column: 04
High quality sequence stop: 659.
Location/Qualifiers
1. .817
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/clone_lib="NIH MGC 67"
/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."

Query Match 27.6%; Score 517.4; DB 12; Length 817;
Best Local Similarity 99.8%; Pred. No. 2.1e-91;
Matches 518; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1358 GGGACCCGAGCTGGCCAGATCCTGGAGAGGTCCGTACATTCGCAATCGCTTCGGT 1417
Db 1 GGGACCCGAGCTGGCCAGATCCTGGAGAGGTCCGTACATTCGCAATCGCTTCGGT 60
QY 1418 GCCAGACGAACCGAGCGGTCTGCAGGAGTGAAGTTCGCCGCTGTGTGGTGACC 1477
Db 61 GCCAGACGAACCGAGCGGTCTGCAGGAGTGAAGTTCGCCGCTGTGTGGTGACC 120
QY 1478 GCTGTGCTCATGGCTTCTCGGTCTTCCACCATCATCGCACCATCGCATCTGATGT 1537
Db 121 GCTGTGCTCATGGCTTCTCGGTCTTCCACCATCATCGCACCATCGCATCTGATGT 180
QY 1538 CGGCTCCCAACTCGTGGAGGCGGTGTCCAAAGACTTTTCGCTAAACACGCTGGTCTGT 1597
Db 181 CGGCTCCCAACTCGTGGAGGCGGTGTCCAAAGACTTTTCGCTAAACACGCTGGTCTGT 240
QY 1598 ACATGTGGAAAACTCAAGATGGGCAAGCCTTTGGCTTTGGCGAGATTTGGGGGTGCTAA 1657
Db 241 ACATGTGGAAAACTCAAGATGGGCAAGCCTTTGGCTTTGGCGAGATTTGGGGGTGCTAA 300
QY 1658 TCCAGGACAGCATTACAGCCCAACTCCAGTGTTCCTTCTCGCTGTGCTGTTCG 1717

Db 301 TCAGAGACATATACAGGACCACTCCAGTGTCCCTTCCTGCTGCTAGTGTGTC 360
 QY 1718 TTACGGTTCTTTGTTACTTTAGTAGTAGAATCTAGACTTTGTTTCAATATCTCAGA 1777
 Db 361 TTACGGTTCTTTGTTACTTTAGTAGTAGAATCTAGACTTTGTTTCAATATCTCAGA 420
 QY 1778 TGGGCTGATAGATATCTTGGACATCCGATACCATCGTTCAGAGGAGGAGGAGTATC 1837
 Db 421 TGGGCTGATAGATATCTTGGACATCCGATACCATCGTTCAGAGGAGGAGGAGTATC 480
 QY 1838 ATTTTGGCCATTAGCCCACTGCTCTGAAAGCCCTTCGGA 1876
 Db 481 ATTTTGGCCATTAGCCCACTGCTCTGAAAGCCCTTCGGA 519

RESULT 11
 BI963064
 LOCUS
 DEFINITION
 ie62c10.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
 cDNA clone IMAGE:5671315 5' similar to SW:ACH7_HUMAN P36544
 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-7 CHAIN PRECURSOR.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 EST.
 BI963064.1 GI:16337469

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biohp.harvard.edu
 Library was constructed by Dr. Douglas Melton DNA sequencing by:
 Washington University Genome Sequencing Center For information on
 obtaining a clone please contact: Juliana Brown
 (brown@fas.harvard.edu) This sequence now available from the IMAGE
 consortium, for clone orders contact: info@image.llnl.gov
 High quality sequence stop: 429.
 Location/Qualifiers
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 /mol_type="mRNA"
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 /clone="IMAGE:5671315"
 /sex="Both"
 /tissue_type="Islets of Langerhans"
 /dev_stage="Adult"
 /lab_host="PH10B"
 /clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
 /note="Organ: Pancreas; Vector: pSPORL1; Site_1: Not 1;
 Site_2: Sal 1; Starting library constructed using
 SuperScript Plasmid Library kit (Life Technologies). cDNA
 made by oligo-dT priming. Size-selected by column
 fractionation; average insert size 1.08 kb. Library was
 amplified once on solid support and plasmid DNA from
 library was prepared. The library DNA was normalized by
 method #4 from Bonaldo, Lennon, and Soares 1996 Genome
 Research 6:791-806; 0.5 microgram single-stranded library

plasmid DNA was mixed with 5 micrograms PCR product
 representing library inserts and hybridized to an EcoT of
 20 single-stranded (unhybridized) plasmids were isolated
 by hydroxyapatite chromatography and used to make this
 library."

ORIGIN
 Query Match 27.0%; Score 506.4; DB 12; Length 536;
 Best Local Similarity 99.8%; Pred. No. 2.5e-89;
 Matches 507; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1369 TTGGCCAAAGATCCTGGAGAGGTCCTGATACATTGCCAATCGCTTCGGTCCAGGACGAA 1428
 Db 1 TTGGCCAAAGATCCTGGAGAGGTCCTGATACATTGCCAATCGCTTCGGTCCAGGACGAA 60
 QY 1429 AGCGAGCGGTCTGCAGCGAGTGGAAAGTTCCGCCCTGTGTGTCGACCCCTGTGCTC 1488
 Db 61 AGCGAGCGGTCTGCAGCGAGTGGAAAGTTCCGCCCTGTGTGTCGACCCCTGTGCTC 120
 QY 1489 ATGGCCCTTCCTGCTCTTCCACCATCATCTGCACCATCGCATCTCGATGTCGGTCCCAAC 1548
 Db 121 ATGGCCCTTCCTGCTCTTCCACCATCATCTGCACCATCGCATCTCGATGTCGGTCCCAAC 180
 QY 1549 TTGCTGAGGCGGTCTCCAAAGACTTTGCTTAACAGCCCTGTTCTGTACATGTGAAA 1608
 Db 181 TTGCTGAGGCGGTCTCCAAAGACTTTGCTTAACAGCCCTGTTCTGTACATGTGAAA 240
 QY 1609 ACTCACAGATGGGCAAGCGCTTTGGCTTGGCGAGATTGGGGGTGCTAAATCCAGGACAGC 1668
 Db 241 ACTCACAGATGGGCAAGCGCTTTGGCTTGGCGAGATTGGGGGTGCTAAATCCAGGACAGC 300
 QY 1669 ATTACAGCCCACTCCAGTTCCTTTCGGCTGTCAGTCTGCTGCTGCTGCTGCTGCTGCT 1728
 Db 301 ATTACAGCCCACTCCAGTTCCTTTCGGCTGTCAGTCTGCTGCTGCTGCTGCTGCTGCT 360
 QY 1729 TTGTTACTTTAGTAGTAGAATCTCAGACACTTTGTTTTCATATTTCTCAGATGGGCTGATAG 1788
 Db 361 TTGTTACTTTAGTAGTAGAATCTCAGACACTTTGTTTTCATATTTCTCAGATGGGCTGATAG 420
 QY 1789 ATATCTTGGCAGATCCGTACCATCGTTCAGAGGCGCAGTACGTAGTTCATTTTGGCCAT 1848
 Db 421 ATATCTTGGCAGATCCGTACCATCGTTCAGAGGCGCAGTACGTAGTTCATTTTGGCCAT 480
 QY 1849 TAGCCCACTGCTCGAAGCCCTTCGGA 1876
 Db 481 TAGCCCACTGCTCGAAGCCCTTCGGA 508

RESULT 12
 AA706348/c
 LOCUS
 DEFINITION
 aa28h12.s1 Soares parathyroid tumor Nbhpa Homo sapiens cDNA clone
 1240199 3' similar to gb:X70257 NEURONAL ACETYLCHOLINE RECEPTOR
 PROTEIN, ALPHA-7 CHAIN (HUMAN); mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 NC-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgpbs-remail.nih.gov
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 CDNA distribution: NCI-CGAP clone distribution information can be


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Db      121  CGCGCTGCGCTCATGGCCCTTCGGCTTCCACCATCATCTGCACCATCGGCATCCTGATG 180
QY      1537  TCGGCTCCCAACTTCGTGAGGCGGTGCAAGAGCTTTGCGTAAACACGCGCTGTTCTG 1596
Db      181  TCGGCTCCCAACTTCGTGAGGCGGTGCAAGAGCTTTGCGTAAACACGCGCTGTTCTG 240
QY      1597  TACATGTGAAAACTCACAGATGGGCAAGCCCTTTGGCTTGGCGAGATTGGGGGTGCTA 1656
Db      241  TACATGTGAAAACTCACAGATGGGCAAGCCCTTTGGCTTGGCGAGATTGGGGGTGCTA 300
QY      1657  ATCCAGACAGATTACAGCCCAACTCGAGTGTCCCTTCCTGCGCTGTCAGTCGTG 1716
Db      301  ATCCAGACAGATTACAGCCCAACTCGAGTGTCCCTTCCTGCGCTGTCAGTCGTG 360
QY      1717  CTTACGGTTCTTGTGTTTACCTTTAGTAGTAGTAATCTCAGCACCTTTGTTTCATATCTCAG 1776
Db      361  CTTACGGTTCTTGTGTTTACCTTTAGTAGTAGTAATCTCAGCACCTTTGTTTCATATCTCAG 420
QY      1777  ATGGGCTGATAGATATCTTTGGCACATCCGTACCATCGGTACAGAGGCCACTGAGTAGT 1836
Db      421  ATGGGCTGATAGATATCTTTGGCACATCCGTACCATCGGTACAGAGGCCACTGAGTAGT 480
QY      1837  CATTTTGGCC 1846
Db      481  CATTTTGGCC 490

RESULT 14
LOCUS   BG288825
DEFINITION 602388156f1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4517221 5', mRNA sequence.
VERSION  BG288825
KEYWORDS  BG288825.1 GI:13044052
SOURCE    Homo sapiens
ORGANISM  Homo sapiens (human)

REFERENCE
AUTHORS  NIH-MGC http://mgi.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-remail.nih.gov
           Tissue Procurement: ATCC
           cDNA Library Preparation: Life Technologies, Inc.
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LHAM10409 row: o column: 14
           High quality sequence stop: 686.

FEATURES
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             /clone="IMAGE:4517221"
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             /lab_host="DH10B (phage-resistant)"
             /clone_lib="NIH_MGC_93"
             /note="Organ: bladder; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 26.0%; Score 488; DB 12; Length 795;
Best Local Similarity 100.0%; Pred. No. 1.3e-85;
Matches 488; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1389  GGTCCGCTACATTGCCAATTCGCTTCGGTGCAGACGAAAGCGAGCGGTCTGCAGCGA 1448
Db      1    GGTCCGCTACATTGCCAATTCGCTTCGGTGCAGACGAAAGCGAGCGGTCTGCAGCGA 60
QY      1449  GTGGAAGTTCCGCGCTGTGTGTGAGCGCGCTGCTCATGGCCCTTCGGTCTTCCAC 1508
Db      61  GTGGAAGTTCCGCGCTGTGTGTGAGCGCGCTGCTCATGGCCCTTCGGTCTTCCAC 120
QY      1509  CATCATCTGCACCATCGGCATCTGATGTGCGGCTCCCAACTTCGTGGAGGCCGTGTCCTAA 1568
Db      121  CATCATCTGCACCATCGGCATCTGATGTGCGGCTCCCAACTTCGTGGAGGCCGTGTCCTAA 180
QY      1569  AGACTTTGCGTTAAACCAAGCCTGCTGTACATGTGGAATACTCAGATGGGCAAGGCC 1628
Db      181  AGACTTTGCGTTAAACCAAGCCTGCTGTACATGTGGAATACTCAGATGGGCAAGGCC 240
QY      1629  TTTGGCTGGCGAGATTGGGGGTGCTAATCAGGACAGCATTACACGCCCAACTCCAG 1688
Db      241  TTTGGCTGGCGAGATTGGGGGTGCTAATCAGGACAGCATTACACGCCCAACTCCAG 300
QY      1689  TGTTCCTTCTCGGCTCTCAGTCGTGTTGCTTACGGTTCTTTGTTACTTTAGTAGTAGA 1748
Db      301  TGTTCCTTCTCGGCTCTCAGTCGTGTTGCTTACGGTTCTTTGTTACTTTAGTAGTAGA 360
QY      1749  ATCTCAGCACTTTGTTTCATATTTCTCAGATGGGCTGATAGATATCCTTGGCACATCCGTA 1808
Db      361  ATCTCAGCACTTTGTTTCATATTTCTCAGATGGGCTGATAGATATCCTTGGCACATCCGTA 420
QY      1809  CCATCGCTCAGCAGAGGCCACTGAGTAGTTCATTTTGGCCCACTGCTCCCTGGAAAGC 1868
Db      421  CCATCGCTCAGCAGAGGCCACTGAGTAGTTCATTTTGGCCCACTGCTCCCTGGAAAGC 480
QY      1869  CCTTCGGA 1876
Db      481  CCTTCGGA 488

RESULT 15
LOCUS   BQ070018
DEFINITION 5', mRNA sequence.
ACCESSION BQ070018
VERSION    BQ070018.1 GI:19899064
KEYWORDS  EST.
SOURCE     Homo sapiens (human)
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 1080)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-remail.nih.gov
           Tissue Procurement: ATCC
           cDNA Library Preparation: Rubin Laboratory
           DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LICM2089 row: b column: 01
           High quality sequence stop: 142.

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             /tissue_type="neuroblastoma, cell line"
             /lab_host="DH10B (phage-resistant)"

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/clone.lib="NIH_MGC_47"
/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dt priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match	25.9%;	Score 486.8;	DB 13;	Length 1080;
Best Local Similarity	87.0%;	Pred. No. 2.6e-85;		
Matches 569;	Conservative 0;	Mismatches 82;	Indels 3;	Gaps 3;
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QY 62	CGGACTCAACATGGCTCTCGCGGAGGCGCTCTGGCTGGCGGCTGGCGCGCTCGCTCC	121		
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Db 181	AACATCCCTTGAGAGGCCCTCGTGGCCATGACTGCGAACCACTCAACCGACTATTCTTAC	240		
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QY 301	TGGCTCAAAATGCTTGGACAGATCACTATTTTACAGTGGAAATGTGAGAAATCCAGGG	360		
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QY 361	GTGAAGACTGTTGCTTCCAGATGGC- CAGATTGGAAA- CCAGACATTCCTCTCTATA	418		
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QY 599	GGTCCCTGGATCTCAGATCGAGGAGCAGATATCAGTGGCTATATCCCAATG	652		
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Search completed: May 8, 2004, 22:02:57
Job time : 5042 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 20:38:58 ; Search time 836 Seconds
(without alignments)

10165.387 Million cell updates/sec

Title: US-09-703-951A-11

Perfect score: 1876

Sequence: 1 GGCGCAGGCGCAGCCCGG.....TGCTGGAAAGCCCTTCGGA 1876

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2941586 seqs, 2264995651 residues

Total number of hits satisfying chosen parameters: 5883172

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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- 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
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- 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1875.6	100.0	1876	9	US-09-892-985-7
2	1875.6	100.0	1876	15	US-10-349-836-11
3	1801	96.0	2087	16	US-10-352-684A-55
4	1787	95.3	1964	13	US-10-302-172-180
5	1624.4	86.6	1636	16	US-10-434-364-3
6	1543	82.2	1590	10	US-09-954-936-1
7	1498.6	79.9	1571	16	US-10-434-364-23
8	1493.8	79.6	1571	16	US-10-434-364-26
9	1200.6	64.0	1571	16	US-10-434-364-9
10	635.2	33.9	880	16	US-10-434-364-15
11	596.8	31.8	692	16	US-10-434-364-16
12	512.2	27.3	968	15	US-10-106-698-1367
13	405.2	21.6	3700	9	US-09-303-232-3
14	392	20.9	494	16	US-10-434-364-19
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					Sequence 11, Appli
					Sequence 55, Appl
					Sequence 180, App
					Sequence 3, Appli
					Sequence 1, Appli
					Sequence 23, Appl
					Sequence 26, Appl
					Sequence 9, Appli
					Sequence 15, Appl
					Sequence 16, Appl
					Sequence 1367, Ap
					Sequence 3, Appli
					Sequence 19, Appl

15	376	20.0	3109	9	US-09-303-232-5	Sequence 5, Appli
16	362.2	19.3	2664	15	US-10-349-836-1	Sequence 1, Appli
17	345.8	18.4	2068	9	US-09-892-985-1	Sequence 1, Appli
18	304.8	16.2	3496	15	US-10-349-836-5	Sequence 5, Appli
19	296.2	15.8	2886	9	US-09-303-232-1	Sequence 1, Appli
20	294.8	15.7	2374	9	US-09-892-985-5	Sequence 5, Appli
21	292.4	15.6	1584	15	US-10-157-031-91	Sequence 91, Appl
22	291.8	15.6	1908	15	US-10-175-523-52	Sequence 52, Appl
23	291.8	15.6	1908	15	US-10-349-836-3	Sequence 3, Appli
24	291.8	15.6	2015	15	US-10-084-817-297	Sequence 297, App
25	284.6	15.2	1756	9	US-09-892-985-3	Sequence 3, Appli
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27	275.4	14.7	1743	16	US-10-303-198-1	Sequence 1, Appli
28	274.4	14.6	1869	9	US-09-941-179A-10	Sequence 10, Appli
29	264.6	14.1	1665	15	US-10-203-968-3	Sequence 3, Appli
30	264.6	14.1	1915	15	US-10-203-968-6	Sequence 6, Appli
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38	246.8	13.2	1350	15	US-10-156-239-12	Sequence 12, Appl
39	246.8	13.2	1350	15	US-10-199-485-12	Sequence 16, Appl
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41	246.8	13.2	2150	9	US-09-795-693-10	Sequence 10, Appl
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44	239.4	12.8	1896	9	US-09-941-179A-6	Sequence 10042, A
45	231.8	12.4	2077	15	US-10-198-846-10042	

ALIGNMENTS

RESULT 1

US-09-892-985-7
; Sequence 7, Application US/09892985
; Patent No. US20020111463A1
; GENERAL INFORMATION:

APPLICANT: Elliot, Kathryn J.

Ellis, Steven B.

Harbold, Michael M.

TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE

RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Heller Ehrman White & McAuliffe

STREET: 4250 Executive Square, 7th Floor

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: Fast-SEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/892, 985

FILING DATE: 27-Jun-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/217,345

FILING DATE: 21-DEC-98

APPLICATION NUMBER: US 08/467,574

FILING DATE: 05-JUN-95

APPLICATION NUMBER: US 08/466,589,

FILING DATE: 05-JUN-95

APPLICATION NUMBER: US 08/028,031

FILING DATE: 08-MAR-93

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L

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QY 1861 TGGAAAGCCCTTCGGA 1876
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RESULT 3
US-10-352-684A-55
; Sequence 55, Application US/10352684A
; Publication No. US20030215452A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Healy, Aileen
; APPLICANT: Kelly, Nadine S.
; APPLICANT: Kelly, Louise M.
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12303, 13906,
; TITLE OF INVENTION: 15513, 17822, 302, 5677, 194, 14393, 28059, 7366, 12212,
; TITLE OF INVENTION: 1981, 261, 12416, 270, 1410, 137, 1871, 13051, 1847, 1849,
; TITLE OF INVENTION: 15403, 340, 10217, 837, 1761, 8990 OR 13249 MOLECULES
; FILE REFERENCE: MP102-019P1R0NMIM
; CURRENT APPLICATION NUMBER: US/10/352,684A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/354,333
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: US 60/360,258
; PRIOR FILING DATE: 2002-02-28

; PRIOR APPLICATION NUMBER: US 60/364,476
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/375,626
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: US 60/386,494
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/390,965
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: US 60/392,480
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/394,128
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/399,783
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 60/403,221
; PRIOR FILING DATE: 2002-08-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 2087
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (104)...(1612)
US-10-352-684A-55

Query Match 96.0%; Score 1801; DB 16; Length 2087;
Best Local Similarity 99.1%; Pred. No. 0;
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US-10-434-364-3

US-10-434-304 : Sequence 3. Application US/10434364

Publication No. IUS20040009554A1

; Publication No: US20060145000A1
CENTRAL INFORMATION:

; GENERAL INFORMATION:
 NAME: WANG DACHUAN

APPLICANT: WANG, DAGUANG

10 TITLE OF INVENTION: QM-7 AND QT-6 CELLS TRANSFECTED WITH MUTANT CELL

INVENTOR	TITLE OF INVENTION	SURFACE EXPRESSED CHARACTER
1	TITLE OF INVENTION	SURFACE EXPRESSED CHARACTER

TITLE OF INVENTION: THE

FILE REFERENCE: MEMORY-11

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; FILE REFERENCE: MEMORI-11
; CURRENT APPLICATION NUMBER: US/1

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; CURRENT APPLICATION NUMBER: US/10/43
 ; CURRENT FILING DATE: 2003-05-09

; CURRENT FILING DATE: 2003-05

;
PRIOR APPLICATION NUMBER

; PRIOR FILING DATE: 2002-05-

NUMBER OF SEQ

; SOFTWARE: Pat

DOEWITZ.
: SEO ID NO 3

LENGTH: 1636

; LENGTH: 163
TYPE: DNA

Query Match	86.6%	Score 1624.4	DB 16	Length 1636
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Query Match	86.6%	Score 1624.4;	DB 16;	Length 1050;
Best local similarity	99.5%	Pred No. 0;		

Best Local Similarity	99.5%;	Pred: No. 0;
1. Mismatches	7.	Indels
0: Gaps	0:	Gaps

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Db 121 GGCGAGTTCAGAGGAAGCTTTACAAAGGAGCTGGTCAAGAAC TACAA TCCCTTGGAGGG 100

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181 CCCGTGGCCAAATGACTCGCAACCACTCACCGTCTACTTCTCCCTGAGCCTCCTGCAGATC 240

DB TGT


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QY 319 ACAGATCACTATTATACAGTGGAAATGTGTGAGATATATCCAGGGGTGAAGACTGTTTCGTTTC 378
Db 301 ACAGATCACTATTATACAGTGGAAATGTGTGAGATATATCCAGGGGTGAAGACTGTTTCGTTTC 360
QY 379 CCAGATGGCCAGATTTGGAAACCAAGACATTTCTTCTATTAACAGTGTGTGATGAGCGGTTT 438
Db 361 CCAGATGGCCAGATTTGGAAACCAAGACATTTCTTCTATTAACAGTGTGTGATGAGCGGTTT 420
QY 439 GAGCCACATTTCCACACTAAGCTGTGTGTAATTTCTTCTGGGCATTTCCAGTACTCTGCT 498
Db 421 GAGCCACATTTCCACACTAAGCTGTGTGTAATTTCTTCTGGGCATTTCCAGTACTCTGCT 480
QY 499 CCAGGCATTTTCAAGAGTTTCTGCTACATCGATGTACGCTGGTTTCCCTTTTGATGTGAG 558
Db 481 CCAGGCATTTTCAAGAGTTTCTGCTACATCGATGTACGCTGGTTTCCCTTTTGATGTGAG 540
QY 559 CACTGAAAACTGAAGTTTGGTCTGCTGTCTTACCGAGGCTGGTCTTGGATCTGCAGATG 618
Db 541 CACTGAAAACTGAAGTTTGGTCTGCTGTCTTACCGAGGCTGGTCTTGGATCTGCAGATG 600
QY 619 CAGGAGCAGATATCAGTGGCTATATCCCAATGAGATGGGACCTAGTGGGAATCCCC 678
Db 601 CAGGAGCAGATATCAGTGGCTATATCCCAATGAGATGGGACCTAGTGGGAATCCCC 660
QY 679 GGCAGAGGAGTGAAGGTTTCTATGAGTGTCTGAAAGAGCCCTACCCCGATGTCACTTTC 738
Db 661 GGCAGAGGAGTGAAGGTTTCTATGAGTGTCTGAAAGAGCCCTACCCCGATGTCACTTTC 720
QY 739 ACAGTGCACATGCGCGCAGACAGCTTACTATGSCCTCAACCTGCTGATCCCTGTGTG 798
Db 721 ACAGTGCACATGCGCGCAGACAGCTTACTATGSCCTCAACCTGCTGATCCCTGTGTG 780
QY 799 CTCATCTCCGCCCTCGCCCTGCTGTGTCTCTGCTTCTGCTGAGATTCGCGGAGAGAT 858
Db 781 CTCATCTCCGCCCTCGCCCTGCTGTGTCTCTGCTTCTGCTGAGATTCGCGGAGAGAT 840
QY 859 TCCCTGGGGATACAGTCTTACTCTCTCTTACCGTCTTCATGCTCTCTGCTGCTGAGATC 918
Db 841 TCCCTGGGGATACAGTCTTACTCTCTTCTTACCGTCTTCATGCTCTCTGCTGCTGAGATC 900
QY 919 ATGCCCGCAACATCCGATTCGGTACCATGATGAGCCAGTACTTCCGAGCACCATGATC 978
Db 901 ATGCCCGCAACATCCGATTCGGTACCATGATGAGCCAGTACTTCCGAGCACCATGATC 960
QY 979 ATCGTGGGCTCTCGGTGTGTGTGACGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1038
Db 961 ATCGTGGGCTCTCGGTGTGTGTGACGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
QY 1039 GACGGGGGCAAGATGCCCAAGTGGACCAAGAGTCACTCTTCTGAACTGTFGTGCGGTGCT 1098
Db 1021 GACGGGGGCAAGATGCCCAAGTGGACCAAGAGTCACTCTTCTGAACTGTFGTGCGGTGCT 1080
QY 1099 CTSCEAATGAGAGCCCGGGGAGACAGAGTGGCCCGCTGCGCCGCTGCGACACAGCAGCG 1158
Db 1081 CTSCEAATGAGAGCCCGGGGAGACAGAGTGGCCCGCTGCGCCGCTGCGACACAGCAGCG 1140
QY 1159 CGCTGAGCCTGGCCAGTGTGAGATGAGCGCGTGGCGCCGCGCCGCGCCGCGCAACCGG 1218
Db 1141 CGCTGAGCCTGGCCAGTGTGAGATGAGCGCGTGGCGCGCGCCGCGCCGCGCAACCGG 1200
QY 1219 AACCTGCTGTAATCGCTTTCGCGGCTTGGACGCGGTGCACTGTGTTCGCGACCCCGGAC 1278
Db 1201 AACCTGCTGTAATCGCTTTCGCGGCTTGGACGCGGTGCACTGTGTTCGCGACCCCGGAC 1260
QY 1279 TCTGGGATGATGTGGCGCATGGCTGCTCCCCCAACGCAAGATGACCTCTCTGAC 1338
Db 1261 TCTGGGATGATGTGGCGCATGGCTGCTCCCCCAACGCAAGATGACCTCTCTGAC 1320
QY 1339 GCGGGGCAACCCCCCGAGGGGACCCGGACTTGGCCAAAGATCTGGAGGAGGTTCGCTTAC 1398
Db 1321 GCGGGGCAACCCCCCGAGGGGACCCGGACTTGGCCAAAGATCTGGAGGAGGTTCGCTTAC 1380
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QY 1399 ATTGCCAATCGCTTCCGCTCCAGGAGGAAGCGAGGCGGTCTGCAGCGAGTGAAGTTC 1458
Db 1381 ATTGCCAATCGCTTCCGCTCCAGGAGGAAGCGAGGCGGTCTGCAGCGAGTGAAGTTC 1440
QY 1459 GCGGCTGTGTGTGACCGCTGTGCTCATGGCCCTTCTCGGTCTTCCACCATCATCTGC 1518
Db 1441 GCGGCTGTGTGTGACCGCTGTGCTCATGGCCCTTCTCGGTCTTCCACCATCATCTGC 1500
QY 1519 ACCATCGGCATCTCGATGTCTCGCTCCCAACTTCTGTGAGGCGGTGTCCAAAGATTTCGG 1578
Db 1501 ACCATCGGCATCTCGATGTCTCGCTCCCAACTTCTGTGAGGCGGTGTCCAAAGATTTCGG 1560
QY 1579 TAACCAAGCTGTGTCTGTACATGTGGAAGACTCACAGATGGGCAAGGCTTTGGCTTGG 1638
Db 1561 TAACCAAGCTGTGTCTGTACATGTGGAAGACTCACAGATGGGCAAGGCTTTGGCTTGG 1620
QY 1639 CGAGATTTGGGGTGC 1654
Db 1621 CGAGATTTGGGGTGC 1636

RESULT 6
US-09-954-936-1
; Sequence 1, Application US/09954936
; Publication No. US20030073161A1
; GENERAL INFORMATION: Clark A.
; APPLICANT: Briggs, Clark A.
; APPLICANT: Gopalakrishnan, Murali
; APPLICANT: McKenna, David G.
; APPLICANT: Monteggia, Lisa M.
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Sullivan, James P.
; APPLICANT: Touma, Edward
; APPLICANT: Abbott Laboratories
; TITLE OF INVENTION: A VARIANT HUMAN ALPHA 7 ACETYLCHOLINE
; RECEPTOR SUBUNIT, AND METHODS OF PRODUCTION AND USES THEREOF
; FILE REFERENCE: 6017.US.01
; CURRENT APPLICATION NUMBER: US/09/954,936
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 08/771,737
; PRIOR FILING DATE: 1996-12-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1590
; TYPE: DNA
; ORGANISM: homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (9)...(1514)
US-09-954-936-1

Query Match 82.2%; Score 1543; DB 10; Length 1590;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 1555; Conservative 1; Mismatches 21; Indels 0; Gaps 0;

QY 72 CATGGCTGTCTCGCGGAGGCGTGTGCTGGCGTGGCGCGGTGCTTCTGCGAGTGC 131
Db 8 CATGAGGTGTAGCCCGGAGGAGTGTGGTGGCACTGGCAGCATCTCTCTGCGAGTGC 67
QY 132 CCGTCAAGCGAGTTCCAGAGGAAGCTTTTACAAGAGCTGGTCAAGAACTACAATCCCTT 191
Db 68 CCGTCAAGCGAGTTCCAGAGGAAGCTTTTACAAGAGCTGGTCAAGAACTACAATCCCTT 127
QY 192 GGAGAGGCGCGTGGCCAAATGACTCGCAACCACTCAACCGTCTATTTCTCCCTGAGCTCT 251
Db 128 GGAGAGGCGCGTGGCCAAATGACTCGCAACCACTCAACCGTCTATTTCTCCCTGAGCTCT 187
QY 252 GCAGATCATGAGCTGGATGAGAAACCAAGTTTTTAAACCAACATTTGGCTGCAAT 311
Db 188 GCAGATCATGAGCTGGATGAGAAACCAAGTTTTTAAACCAACATTTGGCTGCAAT 247
QY 312 GTCTTGGACAGATCACTATTATTACAGTGGAAATGTGTGACAGATATCCAGGGGTGAAGACTCT 371
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Db 248 GTCTTGACAGATCACTATTATACAGTGAATGTGTGCAATATATCCAGGGGTGAAGACTGT 307
Qy 372 TCGTTTCCAGATGGCCAGATTTCGAAACACAGACATTTCTCTATTAACAGTGTCTGATGA 431
Db 308 TCGTTTCCAGATGGCCAGATTTCGAAACACAGACATTTCTCTATTAACAGTGTCTGATGA 367
Qy 432 GCGTTTGAAGCCGACATTCACATTAACAGTGTCTGATGAATTCCTTCGAGCATTCGCAAGTA 491
Db 368 GCGTTTGAAGCCGACATTCACATTAACAGTGTCTGATGAATTCCTTCGAGCATTCGCAAGTA 427
Qy 492 CTTGCTCCAGGATATTCAGAGTCTCTGATGATGATGATGATGATGATGATGATGATGATGAT 551
Db 428 CTTGCTCCAGGATATTCAGAGTCTCTGATGATGATGATGATGATGATGATGATGATGATGAT 487
Qy 552 TGTGAGCAGCTGCAAACTGAAGTTTGGGTCTCTGATGATGATGATGATGATGATGATGATGAT 611
Db 488 TGTGAGCAGCTGCAAACTGAAGTTTGGGTCTCTGATGATGATGATGATGATGATGATGATGAT 547
Qy 612 GCAGATGAGGAGGAGATATCAGTGGCTATATCCCAATGGAGAAATGGGACCTAGTGGG 671
Db 548 GCAGATGAGGAGGAGATATCAGTGGCTATATCCCAATGGAGAAATGGGACCTAGTGGG 607
Qy 672 AATCCCGGCAAGAGGAGTGAAGTCTCTATGAGTGTGCAAGAGCCCTACCCGATGT 731
Db 608 AATCCCGGCAAGAGGAGTGAAGTCTCTATGAGTGTGCAAGAGCCCTACCCGATGT 667
Qy 732 CACCTTCAAGTACCATGCGCCGAGGACGCTCTACTATGAGTGTGCAAGAGCCCTACCCGATGT 791
Db 668 CACCTTCAAGTACCATGCGCCGAGGACGCTCTACTATGAGTGTGCAAGAGCCCTACCCGATGT 727
Qy 792 CTGTGTGCTATCTCCGCTCTCGCCCTCTGATGATGATGATGATGATGATGATGATGATGAT 851
Db 728 CTGTGTGCTATCTCCGCTCTCGCCCTCTGATGATGATGATGATGATGATGATGATGATGAT 787
Qy 852 GAAGATTTCCCTGGGATAACAGTCTTACTCTCTTACCTCTTCTGATGATGATGATGATGAT 911
Db 788 GAAGATTTCCCTGGGATAACAGTCTTACTCTCTTACCTCTTCTGATGATGATGATGATGAT 847
Qy 912 TGAGATCATGCGCGCAACATCGATTGCGTACCATGATGATGATGATGATGATGATGATGATGAT 971
Db 848 TGAGATCATGCGCGCAACATCGATTGCGTACCATGATGATGATGATGATGATGATGATGATGAT 907
Qy 972 CATGATCATGCGCGCTCTCGTGTGTGAGCGGTGATGATGATGATGATGATGATGATGATGATGAT 1031
Db 908 CATGATCATGCGCGCTCTCGTGTGTGAGCGGTGATGATGATGATGATGATGATGATGATGATGAT 967
Qy 1032 CGACCCCGACGGGGCAAGATGCCCAAGTGGACAGAGTCTATCTTCTGAACTGGTGGCG 1091
Db 968 CGACCCCGACGGGGCAAGATGCCCAAGTGGACAGAGTCTATCTTCTGAACTGGTGGCG 1027
Qy 1092 GTGGTTCTSCGATGAAGAGCCCGGGAGAGCAAGGTGGCGCCCGGCTCTGCGACGACAA 1151
Db 1028 GTGGTTCTSCGATGAAGAGCCCGGGAGAGCAAGGTGGCGCCCGGCTCTGCGACGACAA 1087
Qy 1152 GCAGCGCGCTGACGCTGGCCAGTGTGAGATGAGCGCGGTGGCGCCCGGCTCTGCGACGAC 1211
Db 1088 GCAGCGCGCTGACGCTGGCCAGTGTGAGATGAGCGCGGTGGCGCCCGGCTCTGCGACGAC 1147
Qy 1212 CAAAGGAACTGCTGTATCATCGGCTTCGCGGCTTGGACGCGGTGCACTGTGTGCTCCGAC 1271
Db 1148 CAAAGGAACTGCTGTATCATCGGCTTCGCGGCTTGGACGCGGTGCACTGTGTGCTCCGAC 1207
Qy 1272 CCCCAGCTCTGGGTAGTGTGTGGCGCATGAGCTGTCTCCCGACGAGATGAGACCT 1331
Db 1208 CCCCAGCTCTGGGTAGTGTGTGGCGCATGAGCTGTCTCCCGACGAGATGAGACCT 1267
Qy 1332 CTGACAGCGCGGACACCCCGAGGGGACCCGAGCTTGGCAAGATCTCTGAGGAGGT 1391
Db 1268 CTGACAGCGCGGACACCCCGAGGGGACCCGAGCTTGGCAAGATCTCTGAGGAGGT 1327
Qy 1392 CCGCTACATTTGCAATTCGCTTCGCTGCGAGGACGAAAGCGAGGGGTCTGCGAGGAGTG 1451

Db 1328 CCGTACATTTGCCAACCGCTTCCGCTGCCAGGACGAAAGCGAGCGGTCTGCGAGGAGTG 1387
Qy 1452 GAAAGTTTCGCGCCCTGTGTGTGGACCGCCTGTGCTCATGCGCCTTCTCGGTCTTCCACAT 1511
Db 1388 GAAAGTTTCGCGCCCTGTGTGTGGACCGCCTGTGCTCATGCGCCTTCTCGGTCTTCCACAT 1447
Qy 1512 CATCTGACCATCGGCATCTGATGTCGGTCCCACTTCTGCGAGCGCGGTGTCRAAGA 1571
Db 1448 CATCTGACCATCGGCATCTGATGTCGGTCCCACTTCTGCGAGCGCGGTGTCRAAGA 1507
Qy 1572 CTTTGGCTAACCCAGCCTGCTTCTGTATCATGTGAAACCTCACAGATGGGCAAGGCTTT 1631
Db 1508 CTTTGGCTAACCCAGCCTGCTTCTGTATCATGTGAAACCTCACAGATGGGCAAGGCTTT 1567
Qy 1632 GCGTTGCGGAGATTGG 1648
Db 1568 GCGTTGCGGAGATTGG 1584

RESULT 7

US-10-434-364-23
; Sequence 23, Application US/10434364
; Publication No. US2004009554A1
; GENERAL INFORMATION:

APPLICANT: WANG, DAGUANG
TITLE OF INVENTION: QM-7 AND QM-6 CELLS TRANSFECTED WITH MUTANT CELL
; TITLE OF INVENTION: SURFACE EXPRESSED CHANNEL RECEPTORS AND ASSAYS USING
; FILE REFERENCE: MEMORY-11
; CURRENT APPLICATION NUMBER: US/10/434,364
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 60/378,642
; PRIOR FILING DATE: 2002-05-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 1571
; TYPE: DNA
; ORGANISM: Macaca mulatta
US-10-434-364-23

Query Match 79.9%; Score 1498.6; DB 16; Length 1571;
Best Local Similarity 97.1%; Pred. No. 0;
Matches 1525; Conservative 1; Mismatches 45; Indels 0; Gaps 0;
Qy 67 CTCACATGCGCTCTCGCGGAGGCGTCTGGCTGGCTCTGGCGGCTCTGCTCTGCTGAT 126
Db 1 CTCACATGCGCTCTCGCGGAGGCGTCTGGCTGGCTCTGGCGGCTCTGCTCTGCTGAT 60
Qy 127 GTGTCCCTGCAAGGCGAGTTCACAGGAAGCTTTACAGGAGCTGTCAGAACTACAAT 186
Db 61 GTGTCCCTGCAAGGCGAGTTCACAGGAAGCTTTACAGGAGCTGTCAGAACTACAAT 120
Qy 187 CCCTTGGAGAGCGCGTGGCCAACTGACTCGCAACCTCTACCGCTCTACTTCTCCCTGAGC 246
Db 121 CCCTTGGAGAGCGCGTGGCCAACTGACTCGCAACCTCTACCGCTCTACTTCTCCCTGAGC 180
Qy 247 CTCCTGAGATCATGAGCGTGGATGAGAAACCAAGTTTAAACCAACCAATTTGGCTG 306
Db 181 CTCCTGAGATCATGAGCGTGGATGAGAAACCAAGTTTAAACCAACCAATTTGGCTG 240
Qy 307 CAAATGCTTGGACAGATCACTATTTACAGTGAATGTGTCAGAAATATCCAGGGGTGAAG 366
Db 241 CAAATGCTTGGACAGATCACTATTTACAGTGAATGTGTCAGAAATATCCAGGGGTGAAG 300
Qy 367 ACTGTTCTGTTTCCAGATGGCCAGATTGGAAACCAAGCAATTTCTTCTATAACAGTGT 426
Db 301 ACTGTTCTGTTTCCAGATGGCCAGATTGGAAACCAAGCAATTTCTTCTATAACAGTGT 360
Qy 427 GATGAGCGCTTTGAGCGCACATTCACACTAAGCTGTGTGTAATTTCTTCTGGGCAATTC 486
Db 361 GATGAGCGCTTTGAGCGCACATTCACACTAAGCTGTGTGTAATTTCTTCTGGGCAATTC 420

QY 487 CAGTACCTGCTCCAGGCATATTCAGAGTTCTCTGCTACATCGATGTAAGCTGTTTCCC 546
Db 421 CAGTACCTGCTCCAGGCATATTCAGAGTTCTCTGCTACATCGATGTAAGCTGTTTCCC 480
QY 547 TTGATGTGACGACTGCAAACTGAAGTTTGGTCTCTGCTTACGAGGCTGCTCTTGG 606
Db 481 TTGATGTGACGACTGCAAACTGAAGTTTGGTCTCTGCTTACGAGGCTGCTCTTGG 540
QY 607 GATCTGCAGATGTCAGGAGGAGATATCAGTGGCTATATCCCAATGGAGATGGACCTA 666
Db 541 GATCTGCAGATGTCAGGAGGAGATATCAGTGGCTATATCCCAATGGAGATGGACCTA 600
QY 667 GTGGGAATCCCGGCAAGAGGAGTGAAGTTTCTATGAGTGTGCTCAAAAGAGCCCTACCCC 726
Db 601 GTGGGAATCCCGGCAAGAGGAGTGAAGTTTCTATGAGTGTGCTCAAAAGAGCCCTACCCC 660
QY 727 GATGTACCTTTCACAGTACCATCGCCGCGAGGAGCTCTACTATGGCTCAACCTGCTG 786
Db 661 GATGTACCTTTCACAGTACCATCGCCGCGAGGAGCCCTCTACTAGGCTCAACCTGCTG 720
QY 787 ATCCCTGTGTGCTCATCTCGCCCTCTCGCCCTGCTGTGTTCTCTCTGCTGAGATTC 846
Db 721 ATCCCTGTGTGCTCATCTCGCCCTTGGCTGTGTTCTCTCTGCTGAGATTC 780
QY 847 GGGGAGAAATTCCTCGGGGATAACAGTCTTACTCTCTTACCGTCTCTATGCTGCTC 906
Db 781 GGGGAGAAATTCCTCGGGGATAACAGTCTTACTCTCTCTACCTGTCTCTATGCTGCTC 840
QY 907 GTGGCTGAGATCATCGCCGCAACATCCGATTCGGTACCATGATAGCCGAGTCTGCC 966
Db 841 GTGGCTGAGATCATCGCCGCAACATCTGATTCAGTACCATGATAGCCGAGTCTGCC 900
QY 967 AGCACCATGATCATCTGGGCTCTCGGTGTGTGAGCGGTGATCGTGTGCTGAGTACCAC 1026
Db 901 AGCACCATGATCATCTGGGCTCTCGGTGTGTGAGCGGTGATCGTGTGCTGAGTACCAC 960
QY 1027 CACACGACCCGACGCGGGGCAAGATGCCCAGTGGACAGAGTCAATCTCTGCACTGG 1086
Db 961 CACACGACCCGACGCGGGGCAAGATGCCCAGTGGACAGAGTCAATCTCTGCACTGG 1020
QY 1087 TGCGGTGTGTTCTCGATGAAGAGCCCGGGAGGACAGGTGCGCCGCGCTGCCAG 1146
Db 1021 TGCGGTGTGTTCTCGATGAAGAGCCCGGGAGGATAGGTGCGCCGCGCTGCCAG 1080
QY 1147 CACACGACCCGCTGACGCTGCGAGTGTGGAGATGAGCGCGGTGCGCGCGCGGCC 1206
Db 1081 CACACGACCCGCTGACGCTGCGAGCTGCGACGCTGGAGTGGAGCGCGCGCGCGCT 1140
QY 1207 GCCAGCAACGGGAACTGCTGTGATATCGGCTTCCGCGGCTGACGCGGCTGCACTGTGTC 1266
Db 1141 GCCAGCAACGGGAACTGCTGTGATATCGGCTTCCGCGGCTGACGCGGCTGCACTGTGTC 1200
QY 1267 CCGACCCCGACTCTGGGGTGTGTGCGCGCATGGCTGCTCCCGACGACGATGAG 1326
Db 1201 CCGACCCCGACTCTGGGGTGTGTGCGCGCATGGCTGCTCCCGACGACGAGAG 1260
QY 1327 CACCTCTGACGCGGGGCAACCCCGCGAGGGGACCCGAGCTTGGCCAGATCTCTGGAG 1386
Db 1261 CACCTCTGACGCGGGGCAACCCCGAGGGGACCCGAGCTTGGCCAGATCTCTGGAG 1320
QY 1387 GAGGTCCGCTACATTCGCTTCCGCTGCGTGCAGAGAGAGGAGGGGTCTGCAGC 1446
Db 1321 GAGGTCCGCTTACATCGCAACCGCTTTCGCTGCGAGGACGAAAGCGAGGCGGTCTGCAGC 1380
QY 1447 GAGTGAAGTTGCGCCCTGTGGTGGACCGCTGTGCTCATGCGCTTCTCGGCTTC 1506
Db 1381 GAGTGAAGTTGCGCCCTGTGGTGGACCGCTGTGCTCATGCGCTTCTCGGCTTC 1440
QY 1507 ACCATCATCTGCACCATCTGGCATCTCTGATGTGGCTCCCACTTCGTGGAGGCGGTGTC 1566
Db 1441 ACCATCATCTGCACCATCTGGCATCTCTGATGTGGCTCCCACTTCGTGGAGGCGGTGTC 1500
QY 1567 AAAGACTTTTGGCTAAACACGCTTGTCTGTATCATGTGGAAAACTCACAGATGGCAAGG 1626

Db 1501 AAAGACTTTGGTAAACACGCTTGTCTGTACATGTGGAAAACTCACAGATGGCAAGG 1560
QY 1627 CCTTTGGCTTG 1637
Db 1561 CCTCTGGCTTG 1571
RESULT 8
US-10-434-364-26
; Sequence 26, Application US/10434364
; Publication No. US20040009554A1
; GENERAL INFORMATION:
; APPLICANT: WANG, DAGUANG
; TITLE OF INVENTION: QM-7 AND QM-6 CELLS TRANSFECTED WITH MUTANT CELL
; TITLE OF INVENTION: SURFACE EXPRESSED CHANNEL RECEPTORS AND ASSAYS USING
; TITLE OF INVENTION: THE TRANSFECTED CELLS
; FILE REFERENCE: MEMORY-11
; CURRENT APPLICATION NUMBER: US/10/434,364
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 60/378,642
; PRIOR FILING DATE: 2002-05-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 26
; LENGTH: 1571
; TYPE: DNA
; ORGANISM: Macaca mulatta
US-10-434-364-26
Query Match 79.6%; Score 1493.8; DB 16; Length 1571;
Best Local Similarity 96.9%; Pred. No. 0;
Matches 1522; Conservative 1; Mismatches 48; Indels 0; Gaps 0;
QY 67 CTCACATGCGCTGCTCGCCGGAGGCGCTCTGGCTGGCGCTGGCGCGCTCGCTCTCTGCAC 126
Db 1 CTCACATGCGCTGCTCGCAGGAGGCGCTCTGGCTGGCTCTGGCGCGCTCGCTCTCTGCAT 60
QY 127 GTGTCCCTGCAAGGCGAGTTCAGAGGAAGCTTTTCAAGAGGAGCTGGTCAAGAACTACAAAT 186
Db 61 GTGTCCCTGCAAGGCGAGTTCAGAGGAAGCTTTTCAAGAGGAGCTGGTCAAGAACTACAAAC 120
QY 187 CCCTTGGAGAGCCGCTGCGCAATGACCTCGCAACCACTCACCGTCTACTCTTCCTCCGTGAGC 246
Db 121 CCCTTGGAGAGCCGCTGCGCAATGACCTCGCAACCACTCACCGTCTACTCTTCCTCCGTGAGC 180
QY 247 CTCCTGCGAGATCATGGAAGCTGGATGAGAAGAACTTAAAGTTTAAACCAACCAATTTGGCTG 306
Db 181 CTCCTGCGAGATCATGGAAGCTGGATGAGAAGAACTTAAAGTTTAAACCAACCAATTTGGCTG 240
QY 307 CAAATGTCTTGGACAGATCATTTATTTACAGTGAATGTGTGAGATATCCAGGGGTGAG 366
Db 241 CAAATGTCTTGGACAGATCATTTATTTACAGTGAATGTGTGAGATATCCAGGGGTGAG 300
QY 367 ACTGTTCTGTTTCCAGAGTGGCCAGATTTGGAAACCAAGATTTCTTCTATTAACAGTGTCT 426
Db 301 ACTGTTCTGTTTCCAGAGTGGCCAGATTTGGAAACCAAGATTTCTTCTATTAACAGTGTCT 360
QY 427 GATGAGCGCTTTGAGCGCCACATTTCCACACTAACTGTTGGTGAATTTCTTCTGGGCAATTC 486
Db 361 GATGAGCGCTTTGAGCGCCACATTTCCACACTAACTGTTGGTGAATTTCTTCTGGGCAATTC 420
QY 487 CAGTACCTGCTCCAGGCAATATTCAGAGTTCCTGCTACATCGATGTAGCTGGTTCCTCC 546
Db 421 CAGTACCTGCTCCAGGCAATATTCAGAGTTCCTGCTACATCGATGTAGCTGGTTCCTCC 480
QY 547 TTTGATGTGACACTGCAACTGCAACTGCAACTGCAACTGCAACTGCAACTGCAACTGCAACTG 606
Db 481 TTTGATGTGACACTGCAACTGCAACTGCAACTGCAACTGCAACTGCAACTGCAACTGCAACTG 540
QY 607 GATCTGCAGATGTCAGGAGGAGATATCAGTGGCTATATCCCAATGGAGATGGACCTA 666
Db 541 GATCTGCAGATGTCAGGAGGAGATATCAGTGGCTATATCCCAATGGAGATGGACCTA 600

; SEQ ID NO 16
; LENGTH: 692
; TYPE: DNA
; ORGANISM: Macaca mulatta
US-10-434-364-16

Query Match 31.8%; Score 596.8; DB 16; Length 692;
Best Local Similarity 96.2%; Pred. No. 4.6e-170; Indels 0; Gaps 0;
Matches 610; Conservative 1; Mismatches 23;

QY 500 CAGGATATTCAGAGTTCCTCTACATCATGATGAGTGTGTTCCCTTTGATGTCAGC 559
Db 59 CGGGATATTCAGAGTTCCTCTACATCATGAGTGTGCGCGTTTCCTTTGATGTCAGC 118
QY 560 ACTGAAAATGAGTTTGGTCTGTCTATCATGATGAGTGTGTTCCCTTTGATGTCAGC 619
Db 119 ATTGAAAATGAGTTTGGTCTGTCTATCATGATGAGTGTGTTCCCTTTGATGTCAGC 178
QY 620 AGGAGCAGATATCAGTGGCTATATCCCAATGGAGATGGGACCTAGTGGGAATCCCG 679
Db 179 AGGAGCAGATATCAGTGGCTATATCCCAATGGAGATGGGACCTAGTGGGAATCCCG 238
QY 680 GCAAGAGAGTGAAGAGTTCTATGAGTGTGCTGCAAGAGCCCTACCCGATGTCACTTCA 739
Db 239 GCAAGAGAGTGAAGAGTTCTATGAGTGTGCTGCAAGAGCCCTACCCGATGTCACTTCA 298
QY 740 CAGTACCATGCGCGGAGAGCCTCTACTATGAGTGTGCTGCAAGAGCCCTACCCGATGTGTC 799
Db 299 CAGTACCATGCGCGGAGAGCCTCTACTATGAGTGTGCTGCAAGAGCCCTACCCGATGTGTC 358
QY 800 TCATCTCGCCCTCGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 859
Db 359 TCATCTCGCCCTCGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 418
QY 860 CCTTGGGGAATAAGTCTTACTCTCTTACTCTCTTACTCTCTTACTCTCTTACTCTCTT 919
Db 419 CCTTGGGGAATAAGTCTTACTCTCTTACTCTCTTACTCTCTTACTCTCTTACTCTCTT 478
QY 920 TGCCCGCAATCCGATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 979
Db 479 TGCCCGCAATCCGATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 538
QY 980 TCGTGGGCTCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1039
Db 539 TCGTGGGCTCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 598
QY 1040 ACGGGGCAAGATCCCAAGTGGACCAAGTGGACCAAGTGGACCAAGTGGACCAAGTGGAC 1099
Db 599 ACGGGGCAAGATCCCAAGTGGACCAAGTGGACCAAGTGGACCAAGTGGACCAAGTGGAC 658
QY 1100 TSCGATGAGAGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1133
Db 659 TSCGATGAGAGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 692

RESULT 12
US-10-106-698-1367

; Sequence 1367, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0

; SEQ ID NO 1367
; LENGTH: 968
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-106-698-1367

Query Match 27.3%; Score 512.2; DB 15; Length 968;
Best Local Similarity 90.1%; Pred. No. 2.4e-144; Indels 7; Gaps 6;
Matches 608; Conservative 6; Mismatches 54;

QY 1198 CGCGCGCGCCAGCAACGGAACCTGCTACATCGGCTTCGCGGCTTCGACGCGCGT 1257
Db 8 CGCGCGCGCGCCAGTACAGGAACTGCTTACCATCTTCGCGCGCGTTCGCGCGCGT 66
QY 1258 CACTGTGTCCCGACCCCGACTCTCGGCTAGTGTGTGCGCGCATGGCTGTCTCCCGACG 1317
Db 67 CACTGTGTCCCGACCCCGACTCTCGGCTAGTGTGTGCGCGCATGGCTGTCTCCCGACG 126
QY 1318 CAGC-ATGAGCACTCTCTGACGCGGCGCAACCCCGAGGGGACCCGACTTGGCCAA 1376
Db 127 CAGGAATGAACACCCCTTAACCGCGCGGCAAAAAACCGAGGGGAACCCGACTTGGCCAA 186
QY 1377 GATCCTGGAGAGTCCGCTACATTCGCAATCGCTTCGCTGCCAGGACAAAGGAGCG 1436
Db 187 AATCCTG--AGAGTCCGCTAATTTGCCAA--NGYKTCGCTGCCA-KACGAAAGCGAGSC 242
QY 1437 GGTCTGACGAGTGGAGTTCGCGCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1496
Db 243 -GTCTGACGAGTGGAGTTCGCGCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 301
QY 1497 CTCGGTCTTCAACATCATCTGCACCATCGCATCCCTGATGTGCGCTCCCAACTTCGTGGA 1556
Db 302 CTCGGTCTTCAACATCATCTGCACCATCGCATCCCTGATGTGCGCTCCCAACTTCGTGGA 361
QY 1557 GCGCGGTCCAAAGACTTTGCGTAACACGACCTGTTCTGTATCATGTGGAATACTCACAG 1616
Db 362 GCGCGGTCCAAAGACTTTGCGTAACACGACCTGTTCTGTATCATGTGGAATACTCACAG 421
QY 1617 ATGGGCAAGGCTTTGCTTGGCGAGATTGGGGGTGCTTAATCAGGACGAGATTACAG 1676
Db 422 ATGGGCAAGGCTTTGCTTGGCGAGATTGGGGGTGCTTAATCAGGACGAGATTACAG 481
QY 1677 CCACACTCCAGTGTTCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1736
Db 482 CCACACTCCAGTGTTCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 541
QY 1737 TTAGTGTAGTAATCTCAGCACTTTTGTTCATATTTCTCAGATGGCTGATAGATATCCTT 1796
Db 542 TTAGTGTAGTAATCTCAGCACTTTTGTTCATATTTCTCAGATGGCTGATAGATATCCTT 601
QY 1797 GGCACATCCGTAACATCGTTCAGGCGGACCACTGAGTAGTCACTTTGCCATTAGCCAC 1856
Db 602 GGCACATCCGTAACATCGTTCAGGCGGACCACTGAGTAGTCACTTTGCCATTAGCCAC 661
QY 1857 TGCGTGGAAAGCCCT 1871
Db 662 TGCGTGGAAAGCCCT 676

RESULT 13
US-09-303-232-3

; Sequence 3, Application US/09303232A
; Patent No. US20020006657A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; TITLE OF INVENTION: Nucleic Acids which encode
; TITLE OF INVENTION: Insect acetylcholine receptor subunits
; FILE REFERENCE: Le A 33 020-Foreign Countries
; CURRENT APPLICATION NUMBER: US/09/303,232A
; CURRENT FILING DATE: 1999-04-30
; EARLIER APPLICATION NUMBER: DE 198 19 829.9
; EARLIER FILING DATE: 1998-05-04
; NUMBER OF SEQ ID NOS: 6

144 ACCCTTGGAGAGGCGCGTGGCCAAATGACTCGCAACCGCTCACCGTCTACTTCTCCCTGA 203
245 GCCTCTGCGAGATCATGGAGCTGGAGTGAAGAACCAAGTTTAAACCAACCAATTTGGC 304
204 GCCTCTGCGAGATCATGGAGCTGGAGTGAAGAACCAAGTTTAAACCAACCAATTTGGC 263
305 TGCAAAATGCTTGGACAGATCACTATTATTACAGTGGAAATGTGTGAGAAATATCCAGGGGTGA 364
264 TGCAAATGCTTGGACAGATCACTATTATTACAGTGGAAATGTGTGAGAAATATCCAGGGGTGA 323
365 AGACTGTTCTTCCAGATGGCGAGATTTGGAACCAAGATTTCTTCTCTATAACAGTG 424
324 AGACTGTTCTTCCAGATGGCGAGATTTGGAACCAAGATTTCTTCTCTATAACAGTG 383
425 CTGATGAGCGCTTTGAGCGCACATTCACACTAACGTTGTTGTAATTTCTTCTGGGCAT 484
384 CGGATGAGCGCTTTGAGCGCACATTCACACTAACGTTGTTGTAATTTCTTCTGGGCAT 443
485 GCCAGTACCTGCCCTCCAGGCATATTCAGAGTTCCCTGCTA 524
444 GCCAGTACCTGCCCTCCAGGCATATTCAGAGTTCCCTGCTA 483

RESULT 15
US-09-303-232-5
; Sequence 5, Application US/09303232A
; Patent No. US20020006657A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; TITLE OF INVENTION: Nucleic Acids which encode
; TITLE OF INVENTION: Insect acetylcholine receptor subunits
; FILE REFERENCE: Le A 33 020-Foreign Countries
; CURRENT APPLICATION NUMBER: US/09/303,232A
; CURRENT FILING DATE: 1999-04-30
; EARLIER APPLICATION NUMBER: DE 198 19 829.9
; EARLIER FILING DATE: 1998-05-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 3109
; TYPE: DNA
; ORGANISM: Heliothis virescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (95)...(1597)
US-09-303-232-5

Query Match 20.0%; Score 376; DB 9; Length 3109;
Best Local Similarity 54.9%; Pred. No. 8.5e-103;
Matches 817; Conservative 1; Mismatches 646; Indels 24; Gaps 3;

QY 114 GTCGCTCTGCAAGCTGTCCTCAAGGCGAGTTCCAGAGGAGCTTTTACAGGAGCTGGT 173
DB 127 GCGTTTGTGTCCTGATCGAGCAAGTCTCTCAGAGAGAGACTTCTGNAACGCTTGT 186
QY 174 CAAGAATAACAATCCCTTGGAGAGCGCGTGGCCAAATGATCGCAACCACTCACCGTCTA 233
DB 187 GCGGAATAACAACCTTGGAGCGAGCGGTGGCCAAAGAGAGCGCAACCGCTAGAGGTGAG 246
QY 234 CTTCTCCCTGAGCTCTCAGATCATGAGCTGGATGAGAGAGACCAAGTTTAAACCA 293
DB 247 GTTCGGCTTGACCTTGCAGCAATCATGACGTGGACGAGAGAAATCAACTACTATTAAAC 306
QY 294 CAACATTTGGCTGCAATGCTTTTGGACAGATCACTATTTACAGTGGAAATGTGTGAGAA 353
DB 307 CAATATATGGCTGCTGTTGAGTGGAAATGACTTAACCTGAGTGGAAAGCAGCGAGTA 366
QY 354 TCCAGGGGTGAAGACTGTTCTGTTTCCAGATGGCCAGATTTGGAACCAAGATTTCTTCT 413
DB 367 TGGCGGGGTCAAGGACTCAGGATCACGCCACCAAGTTGTGGAGCGCGAGCGTCTTAT 426
QY 414 CTATAACAGTGTGAGAGCGCTTTTGACGCCCACTTCCACACTAACGTTGTGTGAAATTC 473

DB 427 GTATAATAGTGTGACGAGGGTTTGTACGGGACCTTACACAGACCAACGTTGGTGTGAGAAG 486
QY 474 TTCTGGGCATGTCAGTACTGCTCTCCAGGCATATTCAAGAGTTCTCTGTACATCATGTGT 533
DB 487 CGCGGCGAGTTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 546
QY 534 AGCTGTTTCCCTTGTGATGTGAGACACTGCAAACTGAAGTTTGGTCTGCTGCTTACCG 593
DB 547 CGCGTGGTTTCCCTTGTGAGACCAACACTGTGATATGAAGTTTGGTGTGAGTGTGAGT 606
QY 594 AGCTGTTTCCCTTGTGATGTGAGACCAACACTGTGATATGAAGTTTGGTGTGAGTGTGAGT 644
DB 607 CGCAATATGAGTGTGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 666
QY 645 CCCCAATGAGAGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 704
DB 667 AACCAATGAGAGTGTGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 726
QY 705 GTGCTGAAAGAGCTTCCCTTGTGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 764
DB 727 GTGCTGCGCGAGCGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 786
QY 765 CTACTATGGCTCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 824
DB 787 GTACTACTTCTTCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 846
QY 825 GTTCTGCTTCTGCTGAGATTTCCCGGAGAGAGATTTCCCTGCGGATACAGTCTTACTCTC 884
DB 847 CTTTACACTGCCACAGACTCCCGAGAGAGAACTCACACTTGGAGTCACTATTCTTCTTATC 906
QY 885 TCTTACCGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 944
DB 907 GCTGACGCTGCTTCTTCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 966
QY 945 ATTGATAGCCAGTACTTCCCGACAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1004
DB 967 CTTGTTAGGAGCTTCTTCAATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1026
QY 1005 GGTGATCGTGTGAGTACCAACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1064
DB 1027 TGTGTTGCTTCTCAATTACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1086
QY 1065 CAGAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1124
DB 1087 AAAATCAGTATTTCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1146
QY 1125 CAAGTGTGCGCGCGCTGCCAGCAACAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1184
DB 1147 GATCACAGGAGAGACTATAATGATGAACACAGGAGTGAAGAGCTGGAACCTGAAGAGAGAG 1206
QY 1185 GAGCGCGTGGCG 1244
DB 1207 GTCGTGCAAGTCTTGTGCTGCGAAATTTTCTAGATATTGATGATGATGATGATGATGATGAT 1266
QY 1245 CTTGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1302
DB 1267 TCGCGCTCTTAAAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1326
QY 1303 GCCTGCTCTCCCGCAGCAGATGAGCACTCTCTGCAAGCGCGCGCGCGCGCGCGCGCGCGCG 1360
DB 1327 CACGATTTTCCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1386
QY 1361 -----ACCGGACTTTGGCCAGATCTCTGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 1409
DB 1387 GGTGAGCCACCATCGCGAGCTGCACTTACTGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 1446
QY 1410 CTTTCCGCTGCCAGGAGAAAGCGAGCGCTGTCTGAGCGAGTGGAAAGTTTCCGCGCTGTGT 1469
DB 1447 GATGAAGAGGCTGATGAGAGAGCGAGCTGATCAGCGACTGGAAGTTTGTGCGCATGT 1506
QY 1470 GGTGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1529

us-09-703-951a-11.rnpb

Wed May 12 09:51:14 2004

Db 1507 TGTGATAGTTTGGCTGTTGCTGTTTCACACTTTTCAACAATCATCGCGACAGTAGCTGT 1566
Qy 1530 CCTGATGTCGGCTCCCAACTTCTGAGGAGGCCGCTGTCCAAAGACTTTGC 1577
Db 1567 CCTGTTATCGGCACCGCATATCATCGTGCAATGAACCAACCACCTGAGC 1614

Search completed: May 9, 2004, 00:10:49
Job time : 845 secs

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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 18:04:23 ; Search time 150 Seconds
(without alignments)
6940.586 Million cell updates/sec

Title: US-09-703-951a-11
Perfect score: 1876
Sequence: 1 GCGCCAGCGCGAGCGCGG.....TGCCTGGAAGCCCTTGGGA 1876

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*
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3: /cgn2_6/prodata/2/ina/6A COMB.seq.*
4: /cgn2_6/prodata/2/ina/6B COMB.seq.*
5: /cgn2_6/prodata/2/ina/6C COMB.seq.*
6: /cgn2_6/prodata/2/ina/6D COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	1875.6	100.0	1876	2	US-08-466-589-7
2	1875.6	100.0	1876	2	US-08-700-636-7
3	1875.6	100.0	1876	3	US-08-467-574-7
4	1875.6	100.0	1876	4	US-09-217-345-7
5	1875.6	100.0	1876	4	US-08-487-596-11
6	1875.6	100.0	1876	4	US-08-660-451A-11
7	1875.6	100.0	1876	4	US-08-892-985-7
8	1543	82.2	1590	4	US-08-771-737-1
9	1543	82.2	1590	4	US-09-954-936-1
10	362.2	19.3	2277	1	US-08-496-855A-1
11	362.2	19.3	2277	4	US-08-487-596-1
12	362.2	19.3	2664	4	US-08-660-451A-1
13	345.8	18.4	2068	4	US-08-466-589-1
14	345.8	18.4	2068	2	US-08-700-636-1
15	345.8	18.4	2068	3	US-08-467-574-1
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17	345.8	18.4	2068	4	US-08-892-985-1
18	304.8	16.2	3496	4	US-08-660-451A-5
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21	294.8	15.7	2374	2	US-08-700-636-5
22	294.8	15.7	2374	3	US-08-467-574-5
23	294.8	15.7	2374	4	US-09-217-345-5
24	294.8	15.7	2374	4	US-08-892-985-5
25	291.8	15.6	1908	4	US-08-660-451A-3
26	284.6	15.2	1756	2	US-08-466-589-3
27	284.6	15.2	1756	2	US-08-700-636-3

28 284.6 15.2 1756 3 US-08-467-574-3 Sequence 3, Appli
29 284.6 15.2 1756 4 US-09-217-345-3 Sequence 3, Appli
30 284.6 15.2 1756 4 US-09-892-985-3 Sequence 3, Appli
31 279 14.9 1654 4 US-08-487-596-3 Sequence 3, Appli
32 275.4 14.7 1743 4 US-08-487-596-9 Sequence 9, Appli
33 275.4 14.7 1743 4 US-08-484-722-1 Sequence 1, Appli
34 275.4 14.7 1743 4 US-08-660-451A-9 Sequence 9, Appli
35 263.2 14.0 2448 4 US-08-487-596-13 Sequence 13, Appli
36 263.2 14.0 2448 4 US-08-660-451A-13 Sequence 13, Appli
37 263.2 14.0 2450 2 US-08-466-589-9 Sequence 9, Appli
38 263.2 14.0 2450 2 US-08-700-636-9 Sequence 9, Appli
39 263.2 14.0 2450 3 US-08-467-574-9 Sequence 9, Appli
40 263.2 14.0 2450 4 US-09-217-345-9 Sequence 9, Appli
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42 261.6 13.9 1521 1 US-08-496-855A-3 Sequence 3, Appli
43 261.6 13.9 1521 2 US-07-938-154-9 Sequence 9, Appli
44 261.6 13.9 1521 5 PCT-US91-02311-9 Sequence 9, Appli
45 253.4 13.5 1915 4 US-08-487-596-17 Sequence 17, Appli

ALIGNMENTS

RESULT 1
US-08-466-589-7
; Sequence 7, Application US/08466589
; Patent No. 5837489
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClaim
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,589
; FILING DATE: June 5, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: March 8, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9950
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1876 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 73..1581
; US-08-466-589-7

Db	1561	GTGTCAAAGACTTTGGGTAAACGCGCTGGTCTGTATCATGTGGAAAACCTCACAGATGG	1520
Qy	1621	GCAAGCGCTTTGGCTTGGCGAGATTTGGGGGTGCTAAATCCAGGACAGCATTTACACGCCAC	1680
Db	1621	GCAAGCGCTTTGGCTTGGCGAGATTTGGGGGTGCTAAATCCAGGACAGCATTTACACGCCAC	1680
Qy	1681	AATCCAGTGTTCCTTCCTCGCTCGCTCAGTCGTGTGCTTACGGTTTCCTTTGTTACTTTTAG	1740
Db	1681	AATCCAGTGTTCCTTCCTCGCTCGCTCAGTCGTGTGCTTACGGTTTCCTTTGTTACTTTTAG	1740
Qy	1741	GTAGTAGAATCTCAGCACTTTGTTTTCATATTTCTCAGATGGGCTGATAGATATCCTTTGGCA	1800
Db	1741	GTAGTAGAATCTCAGCACTTTGTTTTCATATTTCTCAGATGGGCTGATAGATATCCTTTGGCA	1800
Qy	1801	CATCCGTACCATCGGTACAGCAGGGCCACTCAGTAGTCAATTTGCGCCATTAGCCCACTGCC	1860
Db	1801	CATCCGTACCATCGGTACAGCAGGGCCACTCAGTAGTCAATTTGCGCCATTAGCCCACTGCC	1860
Qy	1861	TGGAAGGCCCTTCGGA	1876
Db	1861	TGGAAGGCCCTTCGGA	1876

RESULT 3

US-08-467-574--7	
; Sequence 7, Application US/08467574	
; Patent No. 6022704	
; GENERAL INFORMATION:	
; APPLICANT: Elliot, Kathryn J.	
; APPLICANT: Ellis, Steven B.	
; APPLICANT: Harpold, Michael M.	
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE	
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME	
; NUMBER OF SEQUENCES: 12	
; CORRESPONDENCE ADDRESS:	
; ADDRESSEE: Brown, Martin, Haller & McClaim	
; STREET: 1660 Union Street	
; CITY: San Diego	
; STATE: CA	
; COUNTRY: USA	
; ZIP: 92101-2926	
; COMPUTER READABLE FORM:	
; MEDIUM TYPE: Diskette	
; COMPUTER: IBM Compatible	
; OPERATING SYSTEM: DOS	
; SOFTWARE: FastSEQ Version 1.5	
; CURRENT APPLICATION DATA:	
; APPLICATION NUMBER: US/08/467,574	
; FILING DATE: June 5, 1995	
; CLASSIFICATION: 536	
; PRIOR APPLICATION DATA:	
; APPLICATION NUMBER: US 08/028,031	
; FILING DATE: March 8, 1993	
; ATTORNEY/AGENT INFORMATION:	
; NAME: Seidman, Stephanie L	
; REGISTRATION NUMBER: 33,779	
; REFERENCE/DOCKET NUMBER: 6362-9949	
; TELECOMMUNICATION INFORMATION:	
; TELEPHONE: 619-238-0999	
; TELEFAX: 619-238-0062	
; TELEX:	
; INFORMATION FOR SEQ ID NO: 7:	
; SEQUENCE CHARACTERISTICS:	
; LENGTH: 1876 base pairs	
; TYPE: nucleic acid	
; STRANDEDNESS: both	
; TOPOLOGY: both	
; MOLECULE TYPE: cDNA	
; FEATURE:	
; NAME/KEY: CDS	
; LOCATION: 73..1581	
US-08-467-574-7	

NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9951
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1876 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 73..1581
OTHER INFORMATION: /product= "ALPHA-7 SUBUNIT"
US-08-487-596-11

Query Match 100.0%; Score 1875.6; DB 4; Length 1876;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1876; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	61	CCGGGACTCAACATGCGTCTCGCGGAGGCGTCTGGCTGGCGCTGGCGCGCTCGCTC	120
DB	61	CCGGGACTCAACATGCGTCTCGCGGAGGCGTCTGGCTGGCGCTGGCGCGCTCGCTC	120
QY	121	CTGCAGCTGCTCCCTGCAAGCGAGTCTTCCAGAGGAGCTTTACAGGAGCTGGTCAAGAAC	180
DB	121	CTGCAGCTGCTCCCTGCAAGCGAGTCTTCCAGAGGAGCTTTACAGGAGCTGGTCAAGAAC	180
QY	181	TACAAATCCCTTGAGAGGCGCGTGGCGAATGACTCGCAACCACTCACCGCTCTACTTCC	240
DB	181	TACAAATCCCTTGAGAGGCGCGTGGCGAATGACTCGCAACCACTCACCGCTCTACTTCC	240
QY	241	CTGAGCTCCTGCGAGATCATGGAGCGTGGATGAGAGAACCAAGTTTAAACCAACAACAT	300
DB	241	CTGAGCTCCTGCGAGATCATGGAGCGTGGATGAGAGAACCAAGTTTAAACCAACAACAT	300
QY	301	TGGCTGCAAAATGCTTGGACAGATCACTATTTACAGTGAATGTGTGAGAAATCCAGGG	360
DB	301	TGGCTGCAAAATGCTTGGACAGATCACTATTTACAGTGAATGTGTGAGAAATCCAGGG	360
QY	361	GTGAAGACTGTTGTTTCCAGATGGCGAGATTGGAAACGAGACATTTCTCTATAAC	420
DB	361	GTGAAGACTGTTGTTTCCAGATGGCGAGATTGGAAACGAGACATTTCTCTATAAC	420
QY	421	AGTGTGATGAGCGCTTGGACGACATTCACACTAAAGTGTGGTGAATTTCTTCTGGG	480
DB	421	AGTGTGATGAGCGCTTGGACGACATTCACACTAAAGTGTGGTGAATTTCTTCTGGG	480
QY	481	CATTGCGAGTACCTGCTCCAGGCATATTCAGAGTTTCTGCTACATGATGATGCTGG	540
DB	481	CATTGCGAGTACCTGCTCCAGGCATATTCAGAGTTTCTGCTACATGATGATGCTGG	540
QY	541	TTTCCCTTTGATGTGAGCACTGCAACTGAATTTGGTCTCTTACGGAGGCTGG	600
DB	541	TTTCCCTTTGATGTGAGCACTGCAACTGAATTTGGTCTCTTACGGAGGCTGG	600
QY	601	TCCCTTGATGTGAGATGAGGAGGAGATATTCAGTGGCTATATCCCAATGGAGATGG	660
DB	601	TCCCTTGATGTGAGATGAGGAGGAGATATTCAGTGGCTATATCCCAATGGAGATGG	660
QY	661	GACCTAGTGGAAATCCCGGCAAGAGGAGTGAAGTTCTATGAGTGTGCAAGAGGCC	720
DB	661	GACCTAGTGGAAATCCCGGCAAGAGGAGTGAAGTTCTATGAGTGTGCAAGAGGCC	720
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DB	721	TACCCGATGTCACTTCAAGTGAACATGGCGCGAGAGCGCTTACTATGGCTCAAC	780
QY	781	CTGCTGATCCCTGTGTGCTCATCTCCGCCCTCGCCCTGTGTGTGTTCTGTCTTCTGCA	840
DB	781	CTGCTGATCCCTGTGTGCTCATCTCCGCCCTCGCCCTGTGTGTGTTCTGTCTTCTGCA	840
QY	841	GATTCCGGGAGAGATTTCCTCGGGATACAGTCTTACTCTCTCTCTCTCTCTCTCTCT	900
DB	841	GATTCCGGGAGAGATTTCCTCGGGATACAGTCTTACTCTCTCTCTCTCTCTCTCTCT	900
QY	901	CTGCTCGTGGCTGAGATCATGCCCGCAACATCCGATTCGGTACCAATGATAGCCAGTAC	960
DB	901	CTGCTCGTGGCTGAGATCATGCCCGCAACATCCGATTCGGTACCAATGATAGCCAGTAC	960
QY	961	TTTCGACAGCACCATGATCATCGTGGGCTCTCGGTGGTGGTACCGTATCGTGTGCGAG	1020
DB	961	TTTCGACAGCACCATGATCATCGTGGGCTCTCGGTGGTGGTACCGTATCGTGTGCGAG	1020
QY	1021	TACCAACACACGACCGGAGGAGGAGTCCCAAGTGGACGACAGTATCTCTTCTG	1080
DB	1021	TACCAACACACGACCGGAGGAGGAGTCCCAAGTGGACGACAGTATCTCTTCTG	1080
QY	1081	AACTGCTGCGCTGCTCTSCGAATGAAGAGCGCGGAGGAGCAAGTGGCGCGGCC	1140
DB	1081	AACTGCTGCGCTGCTCTSCGAATGAAGAGCGCGGAGGAGCAAGTGGCGCGGCC	1140
QY	1141	TGCGAGCAACAAGAGCGGCTGCGAGCTGGCGCTGTGTGAGATGAGCGCGCTGGCGCG	1200
DB	1141	TGCGAGCAACAAGAGCGGCTGCGAGCTGGCGCTGTGTGAGATGAGCGCGCTGGCGCG	1200
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DB	1201	CCGCGCGCAGCAAGGAGGAGCTGTACATCGGCTCCGCGGCTGACGCGGTGCGAC	1260
QY	1261	TGTGTCCCAACCCCGACTCTGCGGCTGTGTGGCGCATGGCTGTCTCCCAACGCGAC	1320
DB	1261	TGTGTCCCAACCCCGACTCTGCGGCTGTGTGGCGCATGGCTGTCTCCCAACGCGAC	1320
QY	1321	GATGAGCACTCTGCGAGCGGCGGCAACCCCGGAGGAGGAGCCGAGCTTGGCCAGATC	1380
DB	1321	GATGAGCACTCTGCGAGCGGCGGCAACCCCGGAGGAGGAGCCGAGCTTGGCCAGATC	1380
QY	1381	CTGGAGGAGTCCGCTACATTCGCTTCCGCTGCGAGCAAGAGGAGGCGGCTC	1440
DB	1381	CTGGAGGAGTCCGCTACATTCGCTTCCGCTGCGAGCAAGAGGAGGCGGCTC	1440
QY	1441	TGCAGGAGTGGAGGTTGCGCGCTGTGTGGTGGACCGCTGTGCTCTCATGGCTTCTCG	1500
DB	1441	TGCAGGAGTGGAGGTTGCGCGCTGTGTGGTGGACCGCTGTGCTCTCATGGCTTCTCG	1500
QY	1501	GTCTTCACCATCATCTGACCATTCGGCATCTGTGCGCTCCCACTTCTGTGGAGGCC	1560
DB	1501	GTCTTCACCATCATCTGACCATTCGGCATCTGTGCGCTCCCACTTCTGTGGAGGCC	1560
QY	1561	GTGTCCAAAGACTTTGGTAAACCAACGCTGTGTACATGTGGAATACTCAGATGG	1620
DB	1561	GTGTCCAAAGACTTTGGTAAACCAACGCTGTGTACATGTGGAATACTCAGATGG	1620
QY	1621	GCAAGGCTTTGGCTTGGCGAGATTGGGGGTGCTAATCCAGAGACAGCATTAACGCCAC	1680
DB	1621	GCAAGGCTTTGGCTTGGCGAGATTGGGGGTGCTAATCCAGAGACAGCATTAACGCCAC	1680
QY	1681	AACTCCAGTGTTCCTTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT	1740
DB	1681	AACTCCAGTGTTCCTTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT	1740
QY	1741	GTAGTGAATCTCAGCACTTTGTTTATATTTCTCAGATGGCTGATAGATATCTTGGCA	1800
DB	1741	GTAGTGAATCTCAGCACTTTGTTTATATTTCTCAGATGGCTGATAGATATCTTGGCA	1800
QY	1801	CATCCGTACCATTCGCTCAGCAGGCGCACTGAGTGTGCTATTTGGCCCATTTAGCCACTGCC	1860
DB	1801	CATCCGTACCATTCGCTCAGCAGGCGCACTGAGTGTGCTATTTGGCCCATTTAGCCACTGCC	1860

QY	1861	TGGAAGCCCTTCGGA	1876
Db	1861	TGGAAAGCCCTTCGGA	1876
RESULT 6			
US-08-660-451A-11			
; Sequence 11, Application US/08660451A			
; Patent No. 6524789			
; GENERAL INFORMATION:			
; APPLICANT: Elliott, Kathryn J.			
; APPLICANT: Harbold, Michael M.			
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE			
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME			
; NUMBER OF SEQUENCES: 20			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Brown, Martin, Haller & McClain			
; STREET: 1660 Union Street			
; CITY: San Diego			
; STATE: CA			
; COUNTRY: USA			
; ZIP: 92101-2926			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Diskette			
; COMPUTER: IBM Compatible			
; OPERATING SYSTEM: DOS			
; SOFTWARE: FastSeq Version 1.5			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/660,451A			
; FILING DATE: June 7, 1996			
; CLASSIFICATION: 435			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: 08/484,722			
; FILING DATE: 06/07/95			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Seidman, Stephanie L			
; REGISTRATION NUMBER: 33,779			
; REFERENCE/DOCKET NUMBER: 6362-9370B			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: 619-238-0999			
; TELEFAX: 619-238-0062			
; TELEX:			
; INFORMATION FOR SEQ ID NO: 11:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 1876 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: double			
; TOPOLOGY: linear			
; MOLECULE TYPE: Genomic DNA			
; HYPOTHETICAL: NO			
; ANTI-SENSE: NO			
; FRAGMENT TYPE:			
; FEATURE:			
; NAME/KEY: Coding Sequence			
; LOCATION: 73...1581			
; OTHER INFORMATION: alpha7 human neuronal nicotinic			
; OTHER INFORMATION: acetylcholine receptor			
; NAME/KEY: 5'UTR			
; LOCATION: 1...72			
; OTHER INFORMATION:			
; NAME/KEY: 3'UTR			
; LOCATION: 1582...1876			
; OTHER INFORMATION:			
; US-08-660-451A-11			
Query Match 100.0%; Score 1875.6; DB 4; Length 1876;			
Best Local Similarity 99.9%; Pred. NO. 0;			
Matches 1875; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
QY	1	GGCGCAGGCGCAGGCCCGCGGCACAGCCGACAGCTGGAGCGCGCGGCTCGCTGCAGCT	60

QY 481 CATTGCGAGTACCTGCTCCAGGCAATATTCAAGAGTTCTGCTACATCATGATACGCTGG 540
Db 481 CATTGCGAGTACCTGCTCCAGGCAATATTCAAGAGTTCTGCTACATCATGATACGCTGG 540
QY 541 TTTCCCTTTGANTGTCAGCACTCAAACTGAAGTTTGGGTCCTGGTCTTACGAGGCTGG 600
Db 541 TTTCCCTTTGANTGTCAGCACTCAAACTGAAGTTTGGGTCCTGGTCTTACGAGGCTGG 600
QY 601 TCCTTGAGTCTGAGATGAGGAGGAGATATCAGTGGCTATATCCCAATGAGAGATGG 660
Db 601 TCCTTGAGTCTGAGATGAGGAGGAGATATCAGTGGCTATATCCCAATGAGAGATGG 660
QY 661 GACTAGTGGGAATCCCGGCAAGAGAGAGTCAAGAGTTCTATGAGTCTGCAAGAGCCCC 720
Db 661 GACTAGTGGGAATCCCGGCAAGAGAGAGTCAAGAGTTCTATGAGTCTGCAAGAGCCCC 720
QY 721 TACCCGAGTACCTTTCAAGTGAACATGCGCGGAGGAGCGCTCTACTATGAGCTCAAC 780
Db 721 TACCCGAGTACCTTTCAAGTGAACATGCGCGGAGGAGCGCTCTACTATGAGCTCAAC 780
QY 781 CTGCTGATCCCTGTGTGCTCATCTCCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCA 840
Db 781 CTGCTGATCCCTGTGTGCTCATCTCCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCA 840
QY 841 GATTCCGGGAGAGATTTCCCTGGGATACAGTCTTACTCTCTCTTACCGTCTTCATG 900
Db 841 GATTCCGGGAGAGATTTCCCTGGGATACAGTCTTACTCTCTCTTACCGTCTTCATG 900
QY 901 CTGCTGCTGAGTATGATCCCGGCAACATCCGATTCGATTCGATGATGATGATGATGATG 960
Db 901 CTGCTGCTGAGTATGATCCCGGCAACATCCGATTCGATTCGATGATGATGATGATGATG 960
QY 961 TTCCGCGAGCACCATGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
Db 961 TTCCGCGAGCACCATGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
QY 1021 TACCACCAACGACCCCGGAGGAGAGTCCGATGAGTGGGACGAGTCAATCTCTCTG 1080
Db 1021 TACCACCAACGACCCCGGAGGAGAGTCCGATGAGTGGGACGAGTCAATCTCTCTG 1080
QY 1081 AACTGCTGCGGTGCTTCTGATGAGAGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGG 1140
Db 1081 AACTGCTGCGGTGCTTCTGATGAGAGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGG 1140
QY 1141 TGCCAGACAAAGAGCGCGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1200
Db 1141 TGCCAGACAAAGAGCGCGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1200
QY 1201 CCGCCCGGAGCAACGCGGAACTGCTGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
Db 1201 CCGCCCGGAGCAACGCGGAACTGCTGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
QY 1261 TGTGTCGAGACCCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
Db 1261 TGTGTCGAGACCCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
QY 1321 CATGAGCACTCTCTGCAAGCGGCGCAACCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1380
Db 1321 GATGAGCACTCTCTGCAAGCGGCGCAACCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1380
QY 1381 CTGAGAGGAGTCCGCTCATATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
Db 1381 CTGAGAGGAGTCCGCTCATATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
QY 1441 TCGAGGAGTGAAGTTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
Db 1441 TCGAGGAGTGAAGTTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
QY 1501 GTCTTCACCATCATCTGCAACCTGCGATCTCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
Db 1501 GTCTTCACCATCATCTGCAACCTGCGATCTCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
QY 1561 GTGTCCAAAGACTTTGCGTAAACACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620

Db 1561 GTGTCCAAAGACTTTGCGTAAACACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
QY 1621 GCAAGGCTTTGCTTGGGAGATTTGGGGGTGCTAAATCCAGGACAGCAATTACACGCCAC 1680
Db 1621 GCAAGGCTTTGCTTGGGAGATTTGGGGGTGCTAAATCCAGGACAGCAATTACACGCCAC 1680
QY 1681 AACTCCAGTGTTCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
Db 1681 AACTCCAGTGTTCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
QY 1741 GTAGTAGAATCTCAGCACTTTCTTCAATTTCTCAGATGGCTGATAGATATCTCTTGGCA 1800
Db 1741 GTAGTAGAATCTCAGCACTTTCTTCAATTTCTCAGATGGCTGATAGATATCTCTTGGCA 1800
QY 1801 CATCCGTACCATCCGTCAGCAGGCGCACTGAGTAGTCAATTTGCCCATTTAGGCCACTGCC 1860
Db 1801 CATCCGTACCATCCGTCAGCAGGCGCACTGAGTAGTCAATTTGCCCATTTAGGCCACTGCC 1860
QY 1861 TGAAGAGCCCTTCGGA 1876
Db 1861 TGAAGAGCCCTTCGGA 1876

RESULT 8

US-08-771-737-1
; Sequence 1, Application US/08771737
; Patent No. 6323000
; GENERAL INFORMATION:
; APPLICANT: Briggs, Clark A.
; APPLICANT: Gopalakrishnan, Murali
; APPLICANT: McKenna, David G.
; APPLICANT: Monteggia, Lisa M.
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Sullivan, James P.
; APPLICANT: Touma, Edward
; APPLICANT: Abbott Laboratories
; TITLE OF INVENTION: A VARIANT HUMAN ALPHA 7 ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR SUBUNIT, AND METHODS OF PRODUCTION AND USES THEREOF
; FILE REFERENCE: 6017.US.01
; CURRENT APPLICATION NUMBER: US/08/771,737
; CURRENT FILING DATE: 1996-12-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1590
; TYPE: DNA
; ORGANISM: homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (9)...(1514)
US-08-771-737-1

Query Match 82.2%; Score 1543; DB 4; Length 1590;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 1555; Conservative 1; Mismatches 21; Indels 0; Gaps 0;

QY 72 CATGCGTGTCTGCGCGGAGGCGCTGCTGCGCGCTGCGCGCTGCGCTGCGCTGCGCTGCGCTGCTGCTG 131
Db 8 CATGAGGTGTAGCCCGGAGGAGTGTGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCTG 67
QY 132 CTTCCNAGGCGGAGTTCCAGAGGAGCTTTACAAGGAGCTGCTCAAGAACTACAAATCCCTT 191
Db 68 CTTGCAAGCGGAGTTCCAGAGGAGCTTTACAAGGAGCTGCTCAAGAACTACAAATCCCTT 127
QY 192 GGAGAGGCGCGTGGCCAAATGACTCGCAACCACTACCGCTTACTTCTCCCTGAGCCTCCT 251
Db 128 GGAGAGGCGCGTGGCCAAATGACTCGCAACCACTACCGCTTACTTCTCCCTGAGCCTCCT 187
QY 252 GCAGATCATGAGCGTGGATGAGAGAACCAAGTTTAAACCAACCAATTTGGCTGCAAT 311
Db 188 GCAGATCATGAGCGTGGATGAGAGAACCAAGTTTAAACCAACCAATTTGGCTGCAAT 247

110 CCGGCTCGCTCTCTGCAAGTGTCCCTGCAAGCGAGTTCAGAGGAAGCTTTACAGGAGC 169
Db
302 CCACGGGATTCGCGAGGGAGGCTCGCATACCGAGACTGAGGACCGGCTCTTCAAACACC 361
Qy
170 TGGTCAAGAACTACATCCCTTGGAGAGGCGGTGGCCCAATGACTCGCAACCACTACCG 229
Db
362 TCTTCGGGGGTACAACCGCTGGGGCGCGCCGGGTGCCCAACACTTTCAGACGTGGTATTG 421
Qy
230 TCTACTCTCTCTGAGCTCTCTGAGATCATGAGAGTGGAGAGGAGCAACCAAGTTTAA 289
Db
422 TGGCTTTGGAGCTGTCCATCGCTGAGCTCATGATGTGATGAGAGCAACCAATGATGA 481
Qy
290 CCACCAACATTTGGTGTCAATGTCTTGGACAGATCACTATTTACAGTGGAAATGTGTAG 349
Db
482 CCACCAAGTCTGGCTAAACAGGAGTGGAGGAGTACAACTGGCTGGAAACCCCGCTG 541
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350 AATATCCAGGGGTGAAGACTGTTCCTTTCCAGATGGCCAGATTTGGAAACCAAGACATTC 409
Db
542 AATTTGGCAACATCACATCTCTCAGGGTCCCTTCTGAGATGATCTGGATCCCGGACATTG 601
Qy
410 TTCTCTATAACAGTGTCTGATGAGCGCTTTGAGCGCCACATTCACACTAAAGTGTGGTGA 469
Db
602 TTCTCTACAAATGAGATGGGAGTTTGCAGTGCACCAATGACCAAGGCCCACTCT 661
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470 ATTCTTTGGCAATGCCAGTACCTGCTCCAGGCAATTCAGAGTTTCTCTGTACATCG 529
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662 TCTCACGGGCACTGTGCACTGGGTGCCCCGGGCCATCTACAAGAGCTCTCTGCAGCATCG 721
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530 ATGACGCTGGTTTCCCTTTGATGTGAGCACTGCAAACTGAAGTTTGGTCTGTGT 589
Db
722 AGCTCACCTTCTTCCCTTTGACCAAGAGTGTGCAAGATGAAGTTTGGCTCTGGATT 781
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590 ACGGAGGCTGGTCTTGTGATCTGAGATGTCAGGAG-----GCAGATATCACTGTGCTATA 643
Db
782 ATGCAAGGCCAGATGACACCTGGAGCAGATGGAGCAGACTGTGACCTGAAGACTACT 841
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644 TCCCAATGGGAATGGAGCTTAGTGGGAATCCCGGCAAGAGGAGTGAAGTTCTATG 703
Db
842 GGGAGAGCGGAGTGGGCGCATCGTCAATGCCACGGGACCTTACAACAGCAAGAAATAGC 901
Qy
704 AGTGTGCAAGAGAGCCCTACCCGATGTACCTTACAGTGACATGCGCGCCAGAGGC 763
Db
902 ACTGTGCGCGAGATCTACCCGAGCTCACCTACGCTTGTCTATCCGGCGGCTGCGCGC 961
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764 TCTACTATGGCTCAACCTGCTGATCCCTGTGTGCTCATCTCCGCGCTCTGCGCTGCTGG 823
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962 TCTTTACACCACTCAACCTCATCTCCCTGCTGCTCATCTCTCTGCTCATCTGTGCTGG 1021
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824 TGTTCCTGCTTCTGAGATTCGGGGAGAAATTTCCCTGGGGATAACAGTCTTACTCT 883
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884 CTCTTACCGTCTTCATGCTGCTGCGCTGAGATCATGCGCCCAACATCCGATTCCGTAC 943
Db
1082 CACTCACCGTCTTCTGCTGCTCATCTGAGATCATCCCTGCTCCCTGCTGCTGCTATCC 1141
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944 CATTTAGTACCCAGTACTTCGCGAGCACCATGATCATCTGCGGCTCTCGTGGTGGTGA 1003
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1142 CGCTCATCGCGAGTACTGCTGTTTACCATGATCTTCTGACCTGCTCATCTGCTATCA 1201
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1004 CGGTGATGCTGTGAGTACACCAACACGACCGCGAGAGGAGATGCCCAAGTGA 1063
Db
1202 CGGTCTTCTGCTGATGTGACCAACCGCTTCCCGAGCACCAACATGCGCCCACTGGG 1261
Qy
1064 CCAGATCATCTTCTGATGCTGCGCTGCTTCTGATGAGAGGCGCGGGAGG 1123
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1262 TCGGGGGGCGCTTCTGGGCTGTGTGCGCGGTGCTTCTGATGAACCGGCGCCCAACAC 1321
Qy
1124 ACAAGGTGCGCGCGCTGCGACCAAGCAGCGGCGCTGCAAGCTTGGCGAGTGTGAGA 1183
Db
1322 CGGTGAGCTGTGCAACCCCTTACGCTGAAGCTCAGCCCCCTTATCATCTGCTGGAGA 1381
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1184 TGAGCGCGGTGGCGCGCGCGCGCGCGAGCAACCGGGAACCTGTGTATCATCGGCTTCCGG 1243

1382 GCAACGTGGATGCGGAGGAGGAGGTGGTGGAGGAGGAGACAGATGGGCATGTG 1441
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1244 GCCTGGAGGGGTGCACTGTGTCCGACCCCGACTCTGGGGTGTAGTGTGGCCGATGG 1303
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1442 CAGGTATGTGGCCCCCTCTGTGGGCACTCTCTGAGCCACGCACTGCTGCTGGGG 1501
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1304 CCTGCTCCCCCAGCAGCAGTATGAGCACCTCTCTGACGCGGGGCAACCCCCCGAGGGGACC 1363
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1502 CCTCAGGTCCCAAGGCTGAGGCTCTGTGCAAGGAGGTGAGTGTGCTATC-----AC 1555
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1364 CGGACTTGGCCCAAGATCTGTGAGGAGGTCCGCTACATTTGCCAATGCTTCGCTGCCAGG 1423
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1556 CCCACATGCAAGAGGCACTGGAAGGTGTGCACTACATTTGCCGACCACTCGGCTGTGAGG 1615
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1424 ACGAAGAGGGCGGTCTGACGAGTGAAGTTTCGCGCGCTGTGTGGTGGACCGCTGT 1483
Db
1616 ATGTGACTTTCGTGAGGAGGACTGGAAGTATTTGCCATGTCATCCAGGATCT 1675
Qy
1484 GCCTCATGGCTTCTCGGTCTTCCACCATCATCTGCAACCATCGGCATCTGATGTC 1538
Db
1676 TCCCTGGCTTATTATCATGCTGCTCTCTCTGGGAGCCATCGGCTCTTTCTGCC 1730

RESULT 11
US-08-487-596-1
; Sequence 1, Application US/08487596
; Patent No. 6440681
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND
; TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NEURONAL
; TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESS: Brown, Martin, Haller & McClain
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,596
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US94/02447
; FILING DATE: 08-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,503
; FILING DATE: 08-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,154
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/504,455
; FILING DATE: 03-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9951
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999

TELEFAX: 619-238-0062

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2277 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 166..1755

OTHER INFORMATION: /product= "ALPHA-2 SUBUNIT"

US-08-487-596-1

Query Match

Best Local Similarity 19.3%; Score 362.2; DB 4; Length 2277;

Matches 780; Conservative 0; Mismatches 643; Indels 12; Gaps 2;

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120 CCGGCTCGCTCCTGACGTCCTGCAAGGCGAGTTCCAGAGGAAGCTTTACAGGAGC 361
130 TGGTCAAGAACTACAACTCCCTTGGAGAGCCCGTGGCCAAATGACTGCAACCACTCACG 229
140 TCTTCCGGGCTACAACTCCCTTGGAGAGCCCGTGGCCAAATGACTGCAACCACTCACG 421
150 TCTTCTTCTCCCTGAGCTCTGAGATCATGAGAGTGGATGAGAGAGCAAGCAAGTTTAA 289
160 TGGCTTTTGGACTTCCATGCTCAGCTCATGATGAGAGTGGATGAGAGAGCAAGCAAGT 481
170 CCACCAATTTGGCTGCAATGCTTGGACAGATCACTATTACAGTGAATGTGTCAG 349
180 CCACCAATTTGGCTGCAATGCTTGGACAGATCACTATTACAGTGAATGTGTCAG 541
190 AATATCCAGGGGTGAAGACTGTTGTTCCAGATGAGCCGATTTGGAACCAAGATTC 409
200 ATTTTGGCAATCATCATCTCTCAGGGTCCCTTCTGAGATGATCTGGATCCCGACATT 601
210 TTCTCTATAAGAGTCTGATGAGCGCTTTGAGCGCACATTCACACATCACTGTTGTTGA 469
220 TTCTCTATAAGAGTCTGATGAGCGCTTTGAGCGCACATTCACACATCACTGTTGTTGA 661
230 ATTTCTTGGCATTTGGCTGCAATGCTTGGACAGATCACTATTACAGTGAATGTGTCAG 529
240 TCTCCAGGGCACTGTGACTGGGTGCCCCCGGCATCTCAAGAGCTCCTGCAAGATCG 721
250 ATGACGCTGTTTCCCTTTGATGTCAGACTGCAAACTGAAGTTGGTCTGCTGCTT 589
260 ACCTCACCCTTCTTCCCTTTCAGGAGTGGAGTGAAGTGAAGTTGGCTCCTGGAATT 781
270 ACGGAGGCTGTTCTTGGATCTGCAAGATGTCAGAGTGGAGTGGAGTGGAGTGGAGT 643
280 ATGACAGGCCAAGATCGACCTGGAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 841
290 TCCCCAATGGAGATGGAGCTTAGTGGGAATCCCCCGCAAGAGGAGTGAAGTTCTATG 703
300 GGGAGAGCGGAGTGGGCTCATCGTCAATGCGCACCGGACCTTACACAGCAAGAGTACG 901
310 ATGCTGTCAAGAGCGCTTACCGGATGTCACCTTACAGTACCATGCGCCGCGCAGCGC 763
320 ACTGTGCGCCGAGATCTACCGGAGCTCACCTACAGTACCATGCGCTTCTGTCATCGG 961
330 TCTACTATGGCTCAACCTGCTGATCCCGTGTGCTCATCTCCGCGCTCGCCCTGCTGG 823
340 TCTTCTACACCATCAACCTGCTGATCCCGTGTGCTCATCTCCGCTGCTCATCTGCTGG 1021
350 TGTTCCTGCTTCTGTCAGATTCGCGGAGAAATTTCCCTGGGGATTAACAGTCTTACTCT 883
360 TCTTCTACTGCTCCCTCGACTCGGCGAGAGATCACTGCTGTCATTTGGTGTGCTGT 1081
370 CTCCTTACCGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 943
380 CACTCACCGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1141
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944 CATTGATAGCCAGTACTTTCGCGAGCAGCATGATCATCTGGGCTTCTCGTGGTGTGA 1003
1142 CGCTCATCGCGAGTACTTCTGCTTTCACCATGATCTTCTGTCACCTGTCCATCA 1201
1004 CGGTGATCGTGTGAGTACCAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1063
1202 CCGTCTTCTGCTGATGTCACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1261
1064 CCAGAGTCACTTCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1123
1262 TCGCGGGGGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1321
1124 ACAAGGTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1183
1322 CCGTGTGAGTCTTCCACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1381
1184 TGAGCGCGGTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1243
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1556 CCCACATGCAAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1615
1424 ACAGAAAGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1483
1616 ATGCTGACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1675
1484 GCCTCATGCGCTTCTGCTGCTTCCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1538
1676 TCCTCTGCTGCTTATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1730
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RESULT 12

US-08-660-451A-1

Sequence 1, Application US/08660451A

Patent No. 6524789

GENERAL INFORMATION:

APPLICANT: Elliott, Kathryn J.

APPLICANT: Harpold, Michael M.

TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE

TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brown, Martin, Hallier & McClain

STREET: 1660 Union Street

CITY: San Diego

STATE: CA

COUNTRY: USA

ZIP: 92101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/660,451A

FILING DATE: June 7, 1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/484,722

FILING DATE: 06/07/95

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L

REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9370B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEX:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2664 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: Genomic DNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE:

ORIGINAL SOURCE:

FEATURE:

NAME/KEY: Coding Sequence

LOCATION: 555...2141

OTHER INFORMATION: alpha2 subunit of human neuronal

OTHER INFORMATION: nicotinic acetylcholine receptor

NAME/KEY: 5'UTR

LOCATION: 1...554

OTHER INFORMATION:

NAME/KEY: 3'UTR

LOCATION: 2142...2666

OTHER INFORMATION:

US-08-660-451A-1

Query Match 19.3%; Score 362.2; DB 4; Length 2664;

Best Local Similarity 54.4%; Pred. No. 1.7e-79;

Matches 780; Conservative 0; Mismatches 643; Indels 12; Gaps 2;

QY 110 CGGGTCTGCTGACGCTGTCCTGCAAGGGAGTTCAGAGGAGCTTTACAAAGGAGC 169
DB 691 CACGGCAATGCCGAGGAGGCTCGCATACGAGACTGAGAACCGGCTTTCAACACC 750
QY 170 TGGTCAAGAACTACAAATCCCTTGGAGAGCCCGTGGCCAAATGACTCGCAACCACTCACCG 229
DB 751 TCTTCGGGGCTACAAACCGCTGGCGCGCGCGTGCACCACTTCAGACGTGGTATTG 810
QY 230 TCTACTTCTCCGTGAGCTCTGAGATCATGAGATGAGAGTGAAGAACCAAGTTTAA 289
DB 811 TCGCGTTTGGAGTGTCCATCGCTCAGCTCATGATGTGATGAGAGAACCAATGATGA 870
QY 290 CCACCAACATTTGGCTGCAATGTCTTGGACAGATCACTATTACAGTGGATGTGTGAG 349
DB 871 CCACCAACGTCTGGCTTAAACAGAGTGGAGCGACTACAACTGGCTGGACCCCGCTG 930
QY 350 AATATCCAGGGTGAAGACTGTTCGTTTCCAGATGGCCAGATTTGGAAACCAAGACTTC 409
DB 931 ATTTTGGCAACATCATCTCTCAGGGTCCCTTCTGAGATGATCTGGATCCCGACATTG 990
QY 410 TTCTCTATACAGTGTGATGAGCGTTTGAAGCCACATTCACACTACAGTGTGGTGA 469
DB 991 TTCTCTATACAAATGAGATGGGAGTTTGCAGTGAACCAATGACCAAGGCGCCACTCT 1050
QY 470 ATTCTTCTGGCATTCGCCAGTACCTGCTCCAGGATATTTCAAGAGTTCCTGTACATCG 529
DB 1051 TCTCCAGGGGCACTGTGCACTGGGTGCCCGGCCATCTACAGAGCTCTCTGAGCATCG 1110
QY 530 ATGTAGCGTGGTTCCCTTTGATGTGACAGACTGCAAACTGAAGTTGGGTCTGTGCTTT 589
DB 1111 AGCTACCTTCTTCCCTTTCGACCAAGAGTGAAGTGAAGTTTGGCTCTCGGACTT 1170
QY 590 ACGGAGCTGGTCTTGGATCTGACATGACAGAG-----GCAGATACAGTGGGTATA 643
DB 1171 ATGACAAGGCCAAGATCGACCTGGAGATGGAGCAGACTGTGGACCTGAAGGACTACT 1230
QY 644 TCCCCAATGAGAAATGGGACCTAGTGGGAATCCCGGCAAGAGAGTGAAGATTTCTATG 703
DB 1231 GGGAGAGCGGAGTGGGCCATCTCAATGCCACGGGCACTTACACAGCAAGAGTACG 1290

QY 704 AGTCTGCAAGAGAGCCCTACCCGATGTCACTTTCACAGTGAACCATGCGCGCAGGAGCGC 763
DB 1291 ACTGCTGCGCGAGATCTACCCGAGCTCACTACGCTTGGTCACTCGCGGCTCGCGC 1350
QY 764 TCTACTATGGCTCAACCTGCTGATCCCTGTGTGCTCATCTCCGCTCGCCCTGCTGCTGG 823
DB 1351 TCTTCTACACATCAACCTCATATCCCTGCTGCTCATCTCTGCTGCTACTGTGCTGG 1410
QY 824 TGTTCCTGCTTCTGTCAGATTCGCGGGGAGAAGATTTCCCTGGGGATAACAGTCTTACTCT 883
DB 1411 TCTTCTACCTGCTCCGCTGCTGCGCGGAGAAGATCACTGCTGCTATTCGCTGCTGTG 1470
QY 884 CTCTTACCGTCTTCATGCTGCTGCTGCTGAGATCATGCGCGCAACATTCGATTCGGTAC 943
DB 1471 CACTCACCGTCTTCTGCTGCTCATCATGAGATCATCCCGTCCACCTCGCTGGTCAATCC 1530
QY 944 CATTGATAGCCAGTACTTCGCGAGCACCATGATCATCTGCGGCTCTTCGCTGCTGGTGA 1003
DB 1531 CGCTCATCGCGGAGTACTGCTGTTCACCATGATCTTTCGTCACTGCTGCTGCTGCTGCT 1590
QY 1004 CGGTGATGCTGCTGAGTACCAACACACGACCCCGAGCGGGGCAAGATGCCCAAGTGA 1063
DB 1591 CCGTCTTCTGCTCAATGTGACACCGCTCCCGCAGCACCCACACCATGCCCATGCGG 1650
QY 1064 CCAGAGTCAATCTTCTGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1123
DB 1651 TCGCGGGGGGCTTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1710
QY 1124 ACNAGGTGCGCCCGCTGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1183
DB 1711 CCGTGGAGCTCTGCCACCCCTACCGCTGAAAGCTCAGCCCTCTTATCATCTGCTGCTG 1770
QY 1184 TGAGCGCGTGGCGCGCGCGCGCAGCAACAGGGAACCTGCTGTACATCGCTTCCCGG 1243
DB 1771 GCNAGTGGATGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1830
QY 1244 GCCTGGAGCGGCTGCACTGTGTCCGAGCCCGGACTCTGGGGTAGTGTGTGGCCGATGG 1303
DB 1831 CAGGTCAATGTGGCGCGCTCTGTGGGCACTCTGCGAGCCAGCGGCACCTGCTGCTGCGG 1890
QY 1304 CCTGCTCCCGCAGCAGCATGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1363
DB 1891 CCTAGGTCCCAAGGCTGAGGCTGTGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1944
QY 1364 CGGACTTGGCCAAAGATCTGAGAGGAGTCCGCTACATTCGCAATCGCTTCCGCTGCCAGG 1423
DB 1945 CCCACATGCAGAAAGCACTGGAAGGTGTGCACTACATTCGCGACCCACCTGCGGTCTGAGG 2004
QY 1424 ACGAAGCGAGCGGTCTGCGAGGAGTGAAGTTCGCGGCTGTGTGGTGGAGCCGCTGT 1483
DB 2005 ATGTGACTCTTCGGTGAAGGAGGAGTGAAGTATGTTGCCATGCTGCTGAGAGATCT 2064
QY 1484 GCTCATGCGCTTCTCGGCTTTCACCATCATCTGCAACCATCGGCATCGGCATCTGATGTC 1538
DB 2065 TCCCTGCTGCTTATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2119

RESULT 13

US-08-466-589-1

; Sequence 1, Application US/08466589

; Patent No. 5837489

; GENERAL INFORMATION:

; APPLICANT: Eliot, Kathryn J.

; APPLICANT: Ellis, Steven B.

; APPLICANT: Harpold, Michael M.

; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Brown, Martin, Haller & McClaim

; STREET: 1660 Union Street

; CITY: San Diego

STATE: CA
 COUNTRY: USA
 ZIP: 92101-2926
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/466,589
 FILING DATE: June 5, 1995
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/028,031
 FILING DATE: March 8, 1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Seidman, Stephanie L
 REGISTRATION NUMBER: 33,779
 REFERENCE/DOCKET NUMBER: 6362-9950
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-238-0999
 TELEFAX: 619-238-0062
 TELEX:
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2068 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: both
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 166..1752
 US-08-466-589-1

Query Match 18.4%; Score 345.8; DB 2; Length 2068;
 Best Local Similarity 54.1%; Pred. No. 1.6e-75;
 Matches 776; Conservative 0; Mismatches 644; Indels 15; Gaps 3;

110 CCGCGTGGCTCTCTGCAAGCGGAGTTCACGAGGAGGCTTTTACAGGAGC 169
 302 CCACGGCATTCCTCGAGGAGGCTGCATACCGAGAGTGGAGCGGCTCTTCAACACC 361
 170 TGGTCAAGAACTACATCCCTTGGAGAGCGCGTGGCAATGACTCGCAACCATCCAG 229
 362 TCTTCGGGGGTACAAACCGCTGGGCGCGCGGTGCCCAACACTTTCAGACGTGTGATG 421
 230 TCTACTTCTCCTGAGCCTCTCGAGATCATGGAGCTGGATGAGAAACCAAGTTTAA 289
 422 TGGCTTTGGACTGTCCATCGCTAGCTCATCGATGTGATGAGAGAACCAATGATGA 481
 290 CCACCAACATTGGCTGCAATGCTTGGACAGATCACTATTATACAGTGGAAATGTGTGAG 349
 482 CCACCAACGTCTGGCTAAACAGAGAGTGGAGCGACTACAAACTGGCTGGAAACCCCGCTG 541
 350 AATATCCAGGGGTGAGACTGTCTTTCAGAGTGGCCAGATTGGAAACCCAGACATTC 409
 542 ATTTTGGCAACATCATCTCTCAGGGTCCCTTCTGAGATGATCTGGATCCCGACATG 601
 410 TTCTCTATAACAGTGTGATGAGCGCTTTGAGCGCACATTCACACTAACGTGTGGTGA 469
 602 TTCTCTACACAAANNITGGGAG---TTTGGAGTGGACCCACATGACCAAGGCCACCTCT 658
 470 ATTCTTCTGGGCAATGCGCAGTACCTGCTCCAGGAGGATTTCAAGAGTTCCTGCTACATCG 529
 659 TCTCCAGCGGCACTGTGCACTGGTGGTCCCGCGCCATCTTACAGAGTCTCTGCAAGATCG 718
 530 ATGTACCGTGGTTTCCCTTGTATGTGCACTGCAACTGAAATGGTGGTCTCTGCTCTT 589
 719 AGCTACCTCTTCTCCCTTCGACCGAGCAACTGCAAGATGAAATGGTGGTCTCTGCACT 778
 590 ACGGAGGCTGGTCTCTGGATCTGCAATGCAAGAG-----GCAGATATCACTGGCTATA 643

779 ATGACAAAGCCAAAGATCGACCTGGAGCAGATGAGCAGACTGTGGACCTGAAGGACTACT 838
 644 TCCCAATGGAGATGGGACCTAGTGGGAATCCCGGCAAGAGAGTGAAGTTCTATG 703
 839 GGGAGAGCGGAGTGGGCAATCGTCAATGCCACGCGCACCTACACAGCAAGAGTACG 898
 704 AGTGTGCAAAAGAGCCCTACCCGATGTCACTTCACTGACCTGACCTGCGCCGAGACGC 763
 899 ACTGTGCGCCGAGATCTACCCGAGTCACTACGCTTGTGCTATCCGCGGCTGCGCG 958
 764 TCTACTATGGCCTCAACCTGTGATCCCTGTGTGCTCATCTCCGCGCTTCCGCGCTGCTG 823
 959 TCTTCTACACCATCAACCTCATATCCCTGCTGCTCATCTCTCTGCTCACTGTGCTG 1018
 824 TGTCTCTGCTTCTGCAATTCGGGGAAGATTTCCCTGGGATACAGTCTTACTCT 883
 1019 TCTTCTACCTGCTCCGACTCGGCGAAGATACGCTGTGCTATTTCCGCTGCTCTGT 1078
 884 CTCTTACCGTCTTTCATGCTGCTGCTGAGATCATGCGCGCAACATCCGATTCGGTAC 943
 1079 CACTCACCGTCTTCTGCTGCTCATCTGAGATCATCTGCTCCGCTCCACTCGTGGTATCC 1138
 944 CATTGATAGCCAGTACTTTCGCGAGCACCATGATCATCTGCGGCTCTCTGCTGCTGCTGA 1003
 1139 CGCTCATCGCGAGTACTCTGCTTCCATGATCTTCTGCTCACTGCTGCTCATCTCA 1198
 1004 CGGTGATGCTGCTGAGTACCAACACGACCGCGGCGGAGAGTSCCCAAAGTGA 1063
 1199 CCGTCTTCTGCTCAATGTGACACCGCTTCCCGAGACCCACACCATGCCCCACTGGG 1258
 1064 CCAGAGTCTATCTTCTGAACTGGTGGCGGTGCTTCTTSCGAATGAAGAGCCCGGGAGG 1123
 1259 TGGCGGGGCGCTTCTTGGGCTGTGTGCCCGGTGGCTTCTGATGAACCGGCCCCACAC 1318
 1124 ACAAGGTGCGCCCGGCTTCCACACAAAGCAGCGCGCTGACGCTGCGCAGTGTGAGGA 1183
 1319 CCGTGGAGCTCTGCCACCCCTTACGCTGAAGCTCAGCCCTCTTATCACTGGCTGAGGA 1378
 1184 TGAGCGCGTGGCGCGCGCCCGCCAGCNAACGGGACCTGCTGTATCATCGGCTTCCGCG 1243
 1379 GCAACCTGATGCGGAGGAGGAGTGGTGGAGGAGGAGTGGTGGAGGAGGAGATGGGATGTG 1438
 1244 GCCTGGAGCGCTGCACTGTGCTCCGACCCCGACTCTGGGGTAGTGTGTGGCGCATGG 1303
 1439 CAGGTGATGTGGCGCGCTCTGTGGGCACTCTCTGAGCCACGCGCACTGCTCACTGCGGG 1498
 1304 CTTGCTCCCCACGACGATGAGCACTCTGTCAGCGCGGCGCAACCCCGCGAGGGGAC 1363
 1499 CTTGAGTCCCAAGGCTGAGGCTCTGCTGAGGAGGAGTGGCTGCTGCTATC-----AC 1552
 1364 CGGACTTGGCAAGATCTGAGGAGTCCGCTACATTGGCAATCGCTTCCGCTGCCAGG 1423
 1553 CCCACATGCAAGAGCACTGGAAGTGTGCACTACATTTGCGGACCACTGGGCTGAGG 1612
 1424 ACAGAAAGCGGCGGCTGTCAGCGAGTGGAAAGTTTCGCGGCTGTGTGGTGGAGCGCTGT 1483
 1613 ATGCTGACTCTTCTGCTGAAGGAGTGGAAATGTTGCGCATGCTCATCGACAGATCT 1672
 1484 GCCTCATGGCGCTTCTCGGTCTTACCATCATCTGCAACATCGGATCTCTGATGTC 1538
 1673 TCCTCTGCGCTTTTATCATGCTGCTTCTGCTGGGAGCAATCGGCTCTTCTGCTG 1727

RESULT 14
 US-08-700-636-1
 ; Sequence 1, Application US/08700636
 ; Patent No. 5910582
 ; GENERAL INFORMATION:
 ; APPLICANT: Elliot, Kathryn J.
 ; APPLICANT: Ellis, Steven B.
 ; APPLICANT: Harpold, Michael M.
 ; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
 ; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME

; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
 ; STREET: 444 South Flower Street, Suite 2000
 ; CITY: Los Angeles
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 90071
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/700,636
 ; FILING DATE: 16-JUL-1996
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/028,031
 ; FILING DATE: 08-MAR-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Reiter, Stephen E.
 ; REGISTRATION NUMBER: 31,192
 ; REFERENCE/DOCKET NUMBER: P41 9368
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-546-4737
 ; TELEFAX: 619-546-9392
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2068 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: both
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 166..1752
 ; US-08-700-636-1

Query Match 18.4%; Score 345.8; DB 2; Length 2068;
 Best Local Similarity 54.1%; Pred. No. 1.6e-75;
 Matches 776; Conservative 0; Mismatches 644; Indels 15; Gaps 3;

QY	110	CGCGTCTGCTGACGCTGCTCCCTCAAGGCGAGTTCCAGAGGAAAGCTTTCAAGGAGC 169
DB	302	CAACGCTATGCGCAGGAGGCTCGCATACCGAGCTGAGACCGGCTTTCAACACC 361
QY	170	TGCTCAAGAACTACAAATCCCTTGGAGAGGCCCGTGGCCAAATGACTCGCAACCACTCACCG 229
DB	362	TCTTCCGGGGCTACAACCGCTGGGGCGCGCGCGTGGCCCAACTTCAGACGTGGTGAATTG 421
QY	230	TCTACTTCTCCCTGAGCTCTCGAGATCATGACGTGATGAGATGAGAGAACCAAGTTTAA 289
DB	422	TGGCTTTTGAGCTGTCCATGCTCAGCTCATGATGTGGATGAGAGAACCAATGATGA 481
QY	290	CCACCAACATTTGGCTGCAAAATGCTTTGACAGACATCACTATTATACAGTGGAAATGTCTCAG 349
DB	482	CCACCAACGCTGTGGCTAAACAGAGAGTGGAGCGACTACAACTGCGTGGAAACCCCGCTG 541
QY	350	AATATCAGGGGTGAAGACTGTGTTTCCAGATGGCCAGATTTGGAAACCAAGACTTC 409
DB	542	ATTTTGGCAACATCACTCTCTCAGGGTCCCTTCTGAGATGATCTGGATCCCGACATTG 601
QY	410	TTCTCTATACAGTGTGATGAGCGCTTTTCAGCCCACTTCCACATTAAGTGTGGTGA 469
DB	602	TTCTCTACAAACAAANTTTGGGAG---TTTGAGTGACCCCATGACCAAGGCCCACTCT 658
QY	470	ATTCTTCTGGCATTTGCCAGTACTGCTGCCAGGCATATTCAAGAGTTCTGCTACATCG 529
DB	659	TCTCCAGGCACTGTGCACTGGGTGCCCCGGCCATCTACAGAGCTCTGTCAGCATCG 718
QY	530	ATGTACGCTGGTTTCCCTTTTGTGATGTGAGCACTGCAAACTGCAAACTTGGGTCTCTGCTT 589

DB	719	ACGTCACTTCTTCCCTTTGACACGACGAGAACTGCAAGATGAAGTTTGGCTCTGGACTT 778
QY	590	ACGAGGCTGGTCTTGGATCTGCAGATGCAGGAG-----GCAGATATCAGTGGCTATA 643
DB	779	ATGACAGGCCAAGATCGACTTGGAGCAGATGGAGCAGACTGTGACCTCAAGGACTACT 838
QY	644	TCCCAATGGAGATGGGACCTTAGTGGGAATCCCGGCAAGAGGTGAAGGTTCTATG 703
DB	839	GGGAGAGCGCGAGTGGGCCATCGTCAATGCCACGCGCACCTACAAACAGCAAGATAGC 898
QY	704	AGTGTGCAAAAGAGCCCTTACCCCGATGTCACCTTACAGATGACCATGCGCGCAGAGCG 763
DB	899	ACTGTGCGCGAGATCTACCCCGACGTCACCTAGCCCTTGTCTATCCGGGGTGCCTGCG 958
QY	764	TCTACTATGGCTCAAACTGTGATCCCTCTGTGTCTCATCTCCGCCCTCGCCCTGTGCG 823
DB	959	TCTTCTACACCATCACTCTATCCCTCTGCTCTCATCTCTGCTCTCACTGTGCTGG 1018
QY	824	TGTTCTCTCTTCTGCAATTCGCGGAGAGATTTCCCTGGGGATACAGTCTTACTCT 883
DB	1019	TCTTCTACTGCTCCCTCCGACTGCGCGGAGAGATCACTGTGCAATTTGGGTGCTGT 1078
QY	884	CTCTTACCGTCTTCACTGCTGCTGCTGAGATCATGCCGCAACATCCGATTCGGTAC 943
DB	1079	CACCTACCGCTTCTCTGCTGCTCTCACTGAGATCATCCGCTCCACTGCTGCTCACTCC 1138
QY	944	CATTGATAGCCGACTTTCGCGACACCATGATCATCTCGTGGGCTCTCGGTGGTGA 1003
DB	1139	CGCTCATCGGCGAGTACCTGTGTTTCCATCATGATCTTGTCACTGCTGCTCACTCA 1198
QY	1004	CGGTGATCGTGTGAGTACACACAGACACCGCGAGCGGGGGAAGATGCCAAGTGA 1063
DB	1199	CGGTCTCTGCTCAATGTGAGCACACCGCTCCCGCAGCACCCACACCATGCCCCACTGG 1258
QY	1064	CCAGAGTCACTCTTCTGAACTGCTGCGGTGCTTCTSCGAATGAAGAGCGCCGCGGAGG 1123
DB	1259	TGCGGGGGGCTTCTTGGGCTGTGTGCCCCCGTGTCTGATGAACCGGCCCGCCACAC 1318
QY	1124	ACAAGTGTGCGCGGCTGCGCAGCAACAGCAGCGGCTGTCAGCTGCGGCTGAGTGGAG 1183
DB	1319	CGTGGAGCTTGCACACCCCTTACGCTGAACTCAGCCCTTCTTATCACTGGCTGAGA 1378
QY	1184	TGAGCGCGTGGCGCGCGCGCCCGCAGCAACCGGAACTGCTGTACATCGGCTTCCGG 1243
DB	1379	GCAACGTGATCCGAGGAGAGAGGAGTGTGTGGAGAGGAGGACAGATGGGCATGTG 1438
QY	1244	GCTTGCAGCGCTGCACTGTGCTCCGACCCCGACTCTCTGGGTGAGTGTGTGGCCGCTGG 1303
DB	1439	CAGGTCACTGGCGCCCTCTGTGGGCACTCTGTGAGCCACCGCCACCTGCACTCTGGGG 1498
QY	1304	CCTGCTCCCGCCACGCAAGTACCTCTCTGCAAGCGGGGCAACCCCGGAGGGGAGCC 1363
DB	1499	CCTCAGGTCCCAAGGTGAGGCTCTGCTGAGAGGCTGAGCTGTGCTATC-----AC 1552
QY	1364	CGGACTTGGCCAGATCTCTGGAGAGGTCGGTCTATGTCATCGTTCGGCTGCCAGG 1423
DB	1553	CCACATGCAAGAGGCACTGGAAGGTGCACTACATTTCCCGACCACTCGGCTCTGAGG 1612
QY	1424	ACGMAAGCAGGCGGTCTGCAAGTGAAGTTGCGCGCTGTGTGTGGTGGAGCCGCTGT 1483
DB	1613	ATGTGACTTCTGGTGAAGAGGACTGGAAGTATGTTGGCATGGTTCATCGACAGATCT 1672
QY	1484	GCCTCATGCGCTTCTCGGTCTTCAACCATCATGCAACCATCGGCATCTGATGATGC 1538
DB	1673	TCTCTGCTGTTTATCATGCTGTCTTCTCGGGACCATCGGCTCTTCTTCTGCC 1727

RESULT 15
 US-08-467-574-1
 ; Sequence 1, Application US/08467574
 ; Patent No. 6022704
 ; GENERAL INFORMATION:
 ; APPLICANT: Eliot, Kathryn J.

Job time : 160 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 15:49:02 ; Search time 781 Seconds
(without alignments)
10204.378 Million cell updates/sec

Title: US-09-703-951A-11

Perfect score: 1876

Sequence: 1 GGCGCGAGCGCGAGCGCGG.....TGCCTGGAAGCCCTTCGGA 1876

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_29Jan04.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2003as.*
- 8: Geneseqn2003bs.*
- 9: Geneseqn2003cs.*
- 10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1875.6	100.0	1876	2 AAV12197	Aav12197 Human neu
2	1875.6	100.0	1876	2 AAT48239	Aat48239 Neuronal
3	1875.6	100.0	1876	6 ABS54875	Ab54875 Human neu
4	1875.6	100.0	1876	6 ABV73248	Abv73248 Human neu
5	1875.6	100.0	1876	8 ADA10864	Adal0864 Human neu
6	1787	95.3	1964	6 ABZ11298	Abz11298 Human pol
7	1543	82.2	1590	2 AAV44687	Aav44687 V274T var
8	1508.6	80.4	1509	4 AAC90380	Aac90380 Wild-type
9	1507	80.3	1509	4 AAC90385	Aac90385 Mutant hu
10	1507	80.3	1509	4 AAC90386	Aac90386 Mutant hu
11	1505.4	80.2	1509	3 AAC58395	Aac58395 Human PRO
12	1505.4	80.2	1509	4 AAC90387	Aac90387 Mutant hu
13	1279	68.2	2511	5 AAS79730	Aas79730 DNA encod
14	958.4	51.1	2769	2 AAT59196	Aat59196 Neuronal
15	743.2	39.6	1416	4 AAC90382	Aac90382 Chimeric
16	647	34.5	2101	2 AAT59197	Aat59197 Neuronal
17	512.2	27.3	368	4 AAH34275	Aah34275 Human col
18	405.2	21.6	3700	3 AAZ24476	Aaz24476 H. viresc
19	376	20.0	3109	3 AAZ24477	Aaz24477 H. viresc
20	362.2	19.3	2277	2 AAV12199	Aav12199 Human neu
21	362.2	19.3	2277	2 AAC90387	Aac90387 Alpha 2 s
22	362.2	19.3	2277	6 ABS54870	Ab54870 Human neu
23	362.2	19.3	2277	6 ABV73243	Abv73243 Human neu

24	362.2	19.3	2664	2 AAT48235	Aat48235 Neuronal
25	362.2	19.3	2664	6 ABK92165	Abk92165 Prostate
26	362.2	19.3	2664	8 ADA10854	Adal0854 Human neu
27	362.2	19.3	2664	9 ADC71170	Adc71170 Human 205
28	362.2	19.3	2666	9 ADC71168	Adc71168 Human 205
29	333.4	17.8	337	2 AAX56154	Aax56154 Human alp
30	306.4	16.3	2082	2 AAT59527	Aat59527 Alpha4 su
31	305.6	16.3	936	4 ABL13733	Ab113733 Drosophil
32	304.8	16.2	2082	2 AAT59528	Aat59528 Alpha4 su
33	304.8	16.2	2752	9 ADB78671	Adb78671 Human nic
34	304.8	16.2	2752	9 ADB78670	Adb78670 Human nic
35	304.8	16.2	2752	9 ADB78661	Adb78661 Human nic
36	304.8	16.2	2752	9 ADB78672	Adb78672 Human nic
37	304.8	16.2	2752	9 ADB78663	Adb78663 Human nic
38	304.8	16.2	2752	9 ADB78669	Adb78669 Human nic
39	304.8	16.2	2752	9 ADB78662	Adb78662 Human nic
40	304.8	16.2	2752	9 ADB78673	Adb78673 Human nic
41	304.8	16.2	3343	9 ADE85024	Ad85024 Farnesyl
42	304.8	16.2	3496	2 AAT48237	Aat48237 Neuronal
43	304.8	16.2	3496	8 ADA10858	Adal0858 Human neu
44	303.2	16.2	1809	5 AAS91552	Aas91552 DNA encod
45	303.2	16.2	2752	9 ADB78660	Adb78660 Human nic

ALIGNMENTS

RESULT 1

AAV12197

ID AAV12197 standard; cDNA; 1876 BP.

XX AC AAV12197;

XX DT 14-MAY-1998 (first entry)

XX DE Human neuronal nicotinic acetylcholine receptor alpha-7 subunit cDNA.

XX KW Human; neuronal nicotinic acetylcholine receptor; alpha-7 subunit;

KW brain tissue; screening; NACR; antibody; ds.

XX OS Homo sapiens.

XX FH Key

XX FT CDS

XX FT Location/Qualifiers

XX FT 73..1581

XX FT /*tag= a

XX FT /product= "neuronal nicotinic acetylcholine receptor

XX FT alpha-7 subunit"

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

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XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

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XX FT

XX FT

XX FT

Human neuronal nicotinic acetylcholine receptor subunits and DNA - also transformed cells useful for screening cpds. which modulate activity of the receptor.
Claim 8; Page 78-79; 99pp; English.
The present sequence encodes a human neuronal nicotinic acetylcholine receptor (NACR) subunit. The cells expressing the alpha and/or beta NACR subunits may be used in a method of screening compounds to identify any which modulate the activity of human neuronal NACR. Subunit specific

AAT48239
 ID AAT48239 standard; DNA; 1876 BP.
 XX
 AC AAT48239;
 XX
 DT 09-APR-1997 (first entry)
 XX
 DE Neuronal nicotinic acetylcholine receptor alpha-7 subunit DNA.
 XX
 KW Neuronal nicotinic acetylcholine receptor; nAChR; neurotransmitter;
 KW ligand-gated receptor; ds.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT CDS 73..1581
 FT /*tag= a
 XX
 XX WO9641876-A1.
 XX
 XX 27-DEC-1996.
 XX
 XX 07-JUN-1996; 96WO-US009775.
 XX
 XX 07-JUN-1995; 95US-00484722.
 XX
 XX (SIBI-) SIBIA NEUROSCIENCES INC.
 XX
 XX Elliott KJ, Harpold MM;
 PI
 XX WPI; 1997-065463/06.
 DR P-PSDB; AAW09025.
 XX
 PT Nucleic acids encoding nicotinic acetylcholine receptor sub-units - used
 PT in screening to determine the effect of drugs on the receptor.
 XX
 PS Disclosure; Page 71-73; 108pp; English.
 XX
 CC A DNA sequence (AAT48239) codes for the alpha-7 subunit (AAW09025) of the
 CC human neuronal nicotinic acetylcholine receptor (nAChR). Host cells, esp.
 CC mammalian cells or amphibian oocytes, carrying alpha-7 nucleic acids,
 CC opt. in combination with other alpha and/or beta subunit nucleic acids
 CC (see also AAT48232-38, AAT48240-41), express recombinant nAChR subunits
 CC useful for identifying cpds. that modulate the activity of human nAChRs
 XX
 SQ Sequence 1876 BP; 369 A; 553 C; 531 G; 423 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1875.6; DB 2; Length 1876;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1875; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGC CGCAGGCGCAGGCGCGGCGACAGCCGAGACGTGGAGCGCGCGCTCGCTGAGCT 60
 DB 1 GGC CGCAGGCGCAGGCGCGGCGACAGCCGAGACGTGGAGCGCGCGCTCGCTGAGCT 60
 QY 61 CCGGGACTCAACATGCGCTCTCGCGGAGGCGCTCTGCGCTGCGCGCGCTCGCTC 120
 DB 61 CCGGGACTCAACATGCGCTCTCGCGGAGGCGCTCTGCGCTGCGCGCGCTCGCTC 120
 QY 121 CTGCAAGTGTCCCTGCAAGCGAGTTCAGAGAGAGCTTTACAGAGAGCTGGTCAAGAAC 180
 DB 121 CTGCAAGTGTCCCTGCAAGCGAGTTCAGAGAGAGCTTTACAGAGAGCTGGTCAAGAAC 180
 QY 181 TACAATCCCTTGGAGAGGCGCGTGGCCAAATGACTCGCAACCACTCACCGCTCTACTTCC 240
 DB 181 TACAATCCCTTGGAGAGGCGCGTGGCCAAATGACTCGCAACCACTCACCGCTCTACTTCC 240
 QY 241 CTGAGCCTCTGCGAGATCATGGAGCTGGATGAGAGAACCAAGTTTTAACCAACCAATT 300
 DB 241 CTGAGCCTCTGCGAGATCATGGAGCTGGATGAGAGAACCAAGTTTTAACCAACCAATT 300
 QY 301 TGGCTGCAATGTCTTGGACAGATCACTATTTACAGTGGATGTGTGATATATCCAGGG 360

Db TGGCTGCAATGTCTTGGACAGATCACTATTTACAGTGGATGTGTGATATATCCAGGG 360
 QY GTGAAGACTGTTGTTTCCAGATGGCCAGATTTGGAAACAGACATTTCTCTATTAAC 420
 Db GTGAAGACTGTTGTTTCCAGATGGCCAGATTTGGAAACAGACATTTCTCTATTAAC 420
 QY AGTCTGATGAGCGCTTTGACGCCACATTCACACTAACAGTGTGGTGAATTTCTCTGG 480
 Db AGTCTGATGAGCGCTTTGACGCCACATTCACACTAACAGTGTGGTGAATTTCTCTGG 480
 QY CATTCGAGTACCTGCTCCAGGAGATTTCAAGAGTTCCTGCTACATCATGATGAGCTGG 540
 Db CATTCGAGTACCTGCTCCAGGAGATTTCAAGAGTTCCTGCTACATCATGATGAGCTGG 540
 QY TTTCCCTTTGATGTGAGCACTGCAAACTGAAGTTTGGGTCTCTGCTTACGAGGCTGG 600
 Db TTTCCCTTTGATGTGAGCACTGCAAACTGAAGTTTGGGTCTCTGCTTACGAGGCTGG 600
 QY TCCTTGGATCTGCAGATGCAGAGGAGATATCAGTGGCTATATCCCAATGGAGATGG 660
 Db TCCTTGGATCTGCAGATGCAGAGGAGATATCAGTGGCTATATCCCAATGGAGATGG 660
 QY GACCTAGTGGGAAATCCCGGCAAGAGGAGTGAAGGTTCTATGAGTGTGCTGCAAGAGGCC 720
 Db GACCTAGTGGGAAATCCCGGCAAGAGGAGTGAAGGTTCTATGAGTGTGCTGCAAGAGGCC 720
 QY TACCCCGGATGTACCTTCAAGTACCATGCGCGCAGAGCGCTCTACTATGGCCTCAAC 780
 Db TACCCCGGATGTACCTTCAAGTACCATGCGCGCAGAGCGCTCTACTATGGCCTCAAC 780
 QY CTGCTGATCCCTGTGTGCTCATCTCCGCTCGCCCTGCTGCTGCTGCTGCTGCTGCTGCA 840
 Db CTGCTGATCCCTGTGTGCTCATCTCCGCTCGCCCTGCTGCTGCTGCTGCTGCTGCTGCA 840
 QY GATTCGCGGGAGAGATTTCCCTGCGGATACAGTCTTACTCTCTTACCGTCTTCTG 900
 Db GATTCGCGGGAGAGATTTCCCTGCGGATACAGTCTTACTCTCTTACCGTCTTCTG 900
 QY CTGCTGCTGGCTGAGATCATGCCCAACATCCGATGGTACCAATGATAGCCAGTAC 960
 Db CTGCTGCTGGCTGAGATCATGCCCAACATCCGATGGTACCAATGATAGCCAGTAC 960
 QY TTCGCGCAGACCATGATCATCTGCGGCTCTGCGTGGTGGTACCGTGTGCTGCTGAG 1020
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 QY TACCAACCAACGACCGCGGCGAGATGCCCAAGTGGACAGAGTCACTCTCTTCTG 1080
 Db TACCAACCAACGACCGCGGCGAGATGCCCAAGTGGACAGAGTCACTCTCTTCTG 1080
 QY AACTGTGCGCGTGTCTCTSCGAATGAAGAGCGCGCGGAGAGCAAGGTGCGCGCGCG 1140
 Db AACTGTGCGCGTGTCTCTSCGAATGAAGAGCGCGCGGAGAGCAAGGTGCGCGCGCG 1140
 QY TGGCAGCAACGAGCGCGCTGCGCTGCGCGAGTGTGAGATGAGCGCGCTGGCGCGCG 1200
 Db TGGCAGCAACGAGCGCGCTGCGCTGCGCGAGTGTGAGATGAGCGCGCTGGCGCGCG 1200
 QY CCGCGCGCAGCAAAACCGGAACTGCTGTATCATCTCGGCTTCCGCGGCTGGACGCGTGCAC 1260
 Db CCGCGCGCAGCAAAACCGGAACTGCTGTATCATCTCGGCTTCCGCGGCTGGACGCGTGCAC 1260
 QY TGTGTCCCGACCGCGCTGCGGCTGAGTGTGCGCGCATGCGCTGCTGCTGCTGCTGCTG 1320
 Db TGTGTCCCGACCGCGCTGCGGCTGAGTGTGCGCGCATGCGCTGCTGCTGCTGCTGCTG 1320
 QY GATGAGCACTCTGCAACGCGCGGCAACCGCGCGAGGCGCGCGCTGGCCAGATC 1380
 Db GATGAGCACTCTGCAACGCGCGGCAACCGCGCGAGGCGCGCGCTGGCCAGATC 1380
 QY CTGAGGAGGCTCGCTTACATTTGCAATCGCTTCCGCTGCGAGGACGAAAGAGCGAGGGGTC 1440
 Db CTGAGGAGGCTCGCTTACATTTGCAATCGCTTCCGCTGCGAGGACGAAAGAGCGAGGGGTC 1440

Db	721	TACCCGATGTCACTTTCACAGTGAACAATCGCGCGAGGACGCTCTACTATGAGCCTCAAC	780
QY	781	CTGCTGATCCCTGTGTGCTCATCTCCGCCCTCGCCCTGCTGGTGTTCCTGCTTCCTGCA	840
Db	781	CTGCTGATCCCTGTGTGCTCATCTCCGCCCTCGCCCTGCTGGTGTTCCTGCTTCCTGCA	840
QY	841	GATTCCGGGAGAGAATTTCCTCTGGGATPAACAGTCTTACTCTCTCTTACCGTCTTCATG	900
Db	841	GATTCCGGGAGAGAATTTCCTCTGGGATPAACAGTCTTACTCTCTCTTACCGTCTTCATG	900
QY	901	CTGCTGCTGCTGAGATCATGCCGGAACATCCGATTTCGGTACCATTTGATAGCCAGTAC	960
Db	901	CTGCTGCTGCTGAGATCATGCCCGCAACATCCGATTTCGGTACCATTTGATAGCCAGTAC	960
QY	961	TTGCCAGCACCATGATCATCTGTGGGCTCTCGTGGTGTGACGGGTGATCGTGTCTCAG	1020
Db	961	TTGCCAGCACCATGATCATCTGTGGGCTCTCGTGGTGTGACGGGTGATCGTGTCTCAG	1020
QY	1021	TACACACACAGACCCCGAGCGGGGGAAGATGCCAAGTGGACAGAGTCATCTTCTG	1080
Db	1021	TACACACACAGACCCCGAGCGGGGCAAGATGCCAAGTGGACAGAGTCATCTTCTG	1080
QY	1081	AACGTGTGCGCTGTGTTCTSCGAATGAAGAGCCCGGGAGACAGAAGTGCSCCGGCC	1140
Db	1081	AACGTGTGCGCTGTGTTCTSCGAATGAAGAGCCCGGGAGACAGAAGTGCSCCGGCC	1140
QY	1141	TGCCAGCACAAAGCAGCGCGCTGCAGCCTGGCCAGTGTGAGATGAGCGCGCTGGCGCGG	1200
Db	1141	TGCCAGCACAAAGCAGCGCGCTGCAGCCTGGCCAGTGTGAGATGAGCGCGCTGGCGCGG	1200
QY	1201	CGGCCGCGAGCAACGGGAACCTGTCTGTACAATGCGTTCGCGGCTTGGACGGGTGAC	1260
Db	1201	CGGCCGCGAGCAACGGGAACCTGTCTGTACAATGCGTTCGCGGCTTGGACGGGTGAC	1260
QY	1261	TGTGTCGCGACCCCGACTCTGGGTGTGTGTGGCGCATGCGCTGCTCCGCCACGCAC	1320
Db	1261	TGTGTCGCGACCCCGACTCTGGGTGTGTGTGGCGCATGCGCTGCTCCGCCACGCAC	1320
QY	1321	GATGAGCACCTCTTGACGCGCGGCAACCCCGAGGGGACCCGGACTTTGGCCAAAGATC	1380
Db	1321	GATGAGCACCTCTTGACGCGGGCAACCCCGAGGGGACCCGGACTTTGGCCAAAGATC	1380
QY	1381	CTGAGGAGGTCCGCTACATTGCCAATTCGCTTCGCTGCGAGACGAAACGAGCGGTC	1440
Db	1381	CTGAGGAGGTCCGCTACATTGGCCAAATCGCTTCGCTGCCAGGACGAAACGAGCGGTC	1440
QY	1441	TGCAGCAGTGGAGTTTCGCGCTGTGTGGTGGACCGCTGTGCTCATGGGCTTCTCG	1500
Db	1441	TGCAGCAGTGGAGTTTCGCGCTGTGTGGTGGACCGCTGTGCTCATGGGCTTCTCG	1500
QY	1501	GTCTTCAACCATCTCGACCATCGGCATCTGATGTCGGCTCCCAACTTCGTGGAGGCC	1560
Db	1501	GTCTTCAACCATCTCGACCATCGGCATCTGATGTCGGCTCCCAACTTCGTGGAGGCC	1560
QY	1561	GTGTCCAAAGACTTTGGGTAAACAGCGCTGTGTACATGTGGAAAACTCAAGATGG	1620
Db	1561	GTGTCCAAAGACTTTGGGTAAACAGCGCTGTGTACATGTGGAAAACTCAAGATGG	1620
QY	1621	GCAAGGCTTTGGCTTCGCGAGATTTGGGGGTGCTAATCCAGGACAGCATTACACGCCAC	1680
Db	1621	GCAAGGCTTTGGCTTCGCGAGATTTGGGGGTGCTAATCCAGGACAGCATTACACGCCAC	1680
QY	1681	AACCTCCAGTGTTCCTTCTGGCTGTCAAGTCGTGTGTCTTACCGGTTTCTTTGTACTTTAG	1740
Db	1681	AACCTCCAGTGTTCCTTCTGGCTGTCAAGTCGTGTGTCTTACCGGTTTCTTTGTACTTTAG	1740
QY	1741	GTAGTAGAATCTCAGCACTTTGTTTCATTTCTCAGATGGGCTGATAGATATCCTTGGCA	1800
Db	1741	GTAGTAGAATCTCAGCACTTTGTTTCATTTCTCAGATGGCTGATAGATATCCTTGGCA	1800
QY	1801	CATCCGTACCATCGGTACGAGGCCCATGTAGTAGTCATTTTGGCCATTTAGCCCATGCCC	1860
Db	1801	CATCCGTACCATCGGTACGAGGCCCATGTAGTAGTCATTTTGGCCATTTAGCCCATGCCC	1860

Qy	1861	TGGAAGCCCTTCGA	1876
Db	1861	TGGAAGCCCTTCGA	1876
 RESULT 4			
ABV73248			
ID	ABV73248	standard; cDNA; 1876 BP.	
XX	AC		
XX	ABV73248;		
DD			
DT	22-JAN-2003	(first entry)	
XX			
DE	Human neuronal NACHr alpha7 subunit encoding cDNA.		
XX	Human; neuronal; nicotinic acetylcholine receptor; NACHr; drug screening		
KW	immunohistochemistry; NACHr alpha7 subunit; gene; ss.		
KM			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
CDS	73..1581		
FT	/tag= a		
FT	/product= "NACHr alpha7 subunit"		
FT	/note= "neuronal nicotinic acetylcholine receptor"		
XX			
FN	WO200259266-A2.		
XX			
PD	01-AUG-2002.		
XX			
Pf	29-OCT-2001; 2001WO-US050985.		
XX			
PR	01-NOV-2000; 2000US-00703951.		
XX			
PA	(MERI) MERCK & CO INC.		
XX			
PI	Gillespie A, Claeps BO, Chavez-Noriega LE, Siegel R, Elliott H,		
XX			
DR	WFI; 2002-698532/75.		
DR	P-PSDB; ABS82435.		
XX			
PT	Cell comprising nucleic acids encoding human alpha and beta subunits of neuronal nicotinic acetylcholine receptors, useful for in vitro screening of a drug substance in a test system specific for humans.		
XX			
FS	Example; Page 129-130; 143pp; English.		
XX			
CC	The invention relates to a suitable host cell transfected with an isolated nucleic acid molecule comprising a sequence of nucleotide ribonucleotides that encodes at least one alpha or beta subunit of human neuronal nicotinic acetylcholine receptor (NACHR). The compounds and methods of the present invention, which provide a means to screen synthetic or recombinant receptors and receptor subunits that are substantially free of contamination from many other receptor proteins are useful for observing the effect of a drug substance on a particular subtype to perform in vitro screening of the drug substance in a test system that is specific for humans. The antibodies can be used in immunohistochemistry and for diagnostic and therapeutic applications. The present sequence represents a human neuronal NACHr alpha7 subunit encoding cDNA		

XX	Sequence	1876 BP	369 A	553 C	530 G	423 T	0 U	1 Other	
QQ	Query Match	100.0%	Score	1875.6	DB	6	Length	1876;	
	Best Local Similarity	100.0%	Pred. No.	0					
	Matches 1876;	Conservative	0	Mismatches	0	Indels	0	Gaps	0
QY	1	GGCGCAGGCGCAGGCCCGGCGCACAGCCGAGACGTGGAGCGCGCGGCTCGCTCGAGCT	60						
Db	1	GGCGCAGGCGCAGGCCCGGCGCACAGCCGAGACGTGGAGCGCGCGGCTCGCTCGAGCT	60						
QY	61	CCGGGACTCAACATGTCGGCTGTCGCGCGGAGCGCTCTGGCTGGCGCTGCCCGCGCTCGCTC	120						

|||||
61 CCGGACTCAAATGCGTCTCGCGGAGGCGTCTGCTGCGCTGCGCGTCTGCTC 120
|||||
121 CTGACGCTGCTCTCAAGCGAGTTCAGAGAGAGCTTTACAGAGCTGCTCAAGAAC 180
121 CTGACGCTGCTCTCAAGCGAGTTCAGAGAGAGCTTTACAGAGCTGCTCAAGAAC 180
|||||
181 TACAATCCCTTGGAGAGGCGCGTGGCCAAATGACTCGCAACCACTCAACCGCTACTTCTCC 240
181 TACAATCCCTTGGAGAGGCGCGTGGCCAAATGACTCGCAACCACTCAACCGCTACTTCTCC 240
|||||
241 CTGAGCTCTGAGAGATCATGAGCGTGGATGAGAGAACCAAGTTTAAACCAACCAATTT 300
241 CTGAGCTCTGAGAGATCATGAGCGTGGATGAGAGAACCAAGTTTAAACCAACCAATTT 300
|||||
301 TGCGTCAAAATGCTTGGACAGATCACTATTTACAGTGGATGCTGTCAGAAATATCCAGG 360
301 TGCGTCAAAATGCTTGGACAGATCACTATTTACAGTGGATGCTGTCAGAAATATCCAGG 360
|||||
361 GTGAAGACTGTTCTGTTTCCAGATGCGCAGATTTGGAACCAAGATTTCTCTATAAC 420
361 GTGAAGACTGTTCTGTTTCCAGATGCGCAGATTTGGAACCAAGATTTCTCTATAAC 420
|||||
421 AGTCTGATGAGCGCTTTGAGCGCACATTTCCACATTAACAGTGTGTTGTAATTTCTTGG 480
421 AGTCTGATGAGCGCTTTGAGCGCACATTTCCACATTAACAGTGTGTTGTAATTTCTTGG 480
|||||
481 CATTTGCAATGCTCTGCTCCAGGCAATTTCAAGATTTCTGCTACATGATGATGATGCTGG 540
481 CATTTGCAATGCTCTGCTCCAGGCAATTTCAAGATTTCTGCTACATGATGATGATGCTGG 540
|||||
541 TTTCCCTTTGATGTCAGACTGCAAACTGAAATTTGGGCTCTGCTTTACGAGGCTGG 600
541 TTTCCCTTTGATGTCAGACTGCAAACTGAAATTTGGGCTCTGCTTTACGAGGCTGG 600
|||||
601 TCTTGTGATCTGAGATGAGGAGGAGATATCAGTGGCTATATCCCAATGAGATGAG 660
601 TCTTGTGATCTGAGATGAGGAGGAGATATCAGTGGCTATATCCCAATGAGATGAG 660
|||||
661 GACTAGTGGGAATCCCGGCAAGAGAGTGAAGGTTCTATGAGTCTCTCAAGAGCC 720
661 GACTAGTGGGAATCCCGGCAAGAGAGTGAAGGTTCTATGAGTCTCTCAAGAGCC 720
|||||
721 TACCCGATGTCACCTTCAAGTGAACATGCGCGCAGAGCGCTCTACTATGAGCTCAAC 780
721 TACCCGATGTCACCTTCAAGTGAACATGCGCGCAGAGCGCTCTACTATGAGCTCAAC 780
|||||
781 CTGCTGATCCCTGCTGCTCATCTCGCCCTCGCCCTGCTGCTGCTGCTGCTGCTGCTGCA 840
781 CTGCTGATCCCTGCTGCTCATCTCGCCCTCGCCCTGCTGCTGCTGCTGCTGCTGCTGCA 840
|||||
841 GATTCCGGGAGAGATTTCCCTGGGATAACAGTCTTACTCTCTTACCGTCTTCTCATG 900
841 GATTCCGGGAGAGATTTCCCTGGGATAACAGTCTTACTCTCTTACCGTCTTCTCATG 900
|||||
901 CTGCTGCTGCTGAGATCATGCGCGCAACATCCGATTCGGTACCAATGATAGCCAGTAC 960
901 CTGCTGCTGCTGAGATCATGCGCGCAACATCCGATTCGGTACCAATGATAGCCAGTAC 960
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961 TTGCGCAGCACATGATCATGCTGGGCTCTCGGTGGTGGTGGAGTGGTGGTGGTGGTGG 1020
961 TTGCGCAGCACATGATCATGCTGGGCTCTCGGTGGTGGTGGAGTGGTGGTGGTGGTGG 1020
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1021 TACCACCAACCAAGCGCGGCAAGATGCCCCAAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 1080
1021 TACCACCAACCAAGCGCGGCAAGATGCCCCAAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 1080
|||||
1081 AACTGTGCTGCTGCTGCTTCTTCTGTAAGAGGCGCGGAGGAGCAAGTGGCGCGCGCC 1140
1081 AACTGTGCTGCTGCTGCTTCTTCTGTAAGAGGCGCGGAGGAGCAAGTGGCGCGCGCC 1140
|||||
1141 TGCCAGACACAGCGCGCTGAGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCG 1200

Db 1141 TGCCAGACACAGCGCGCTGAGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCG 1200
Qy 1201 CCGCGCGCAGCAACCGGAACTCTGTGTACATCTGCGCTTCCGCGCTTGAAGCGCTGAC 1260
Db 1201 CCGCGCGCAGCAACCGGAACTCTGTGTACATCTGCGCTTCCGCGCTTGAAGCGCTGAC 1260
Qy 1261 TGTGTCGCGACCCCGACTCTGGGTAGTGTGTGGCGCATGGCTGTCTCCCGCAGCAC 1320
Db 1261 TGTGTCGCGACCCCGACTCTGGGTAGTGTGTGGCGCATGGCTGTCTCCCGCAGCAC 1320
Qy 1321 GATGAGCACCTCTGCGCGGCAACCCCGCGGAGGAGCCCGACTTTGGCCAGATC 1380
Db 1321 GATGAGCACCTCTGCGCGGCAACCCCGCGGAGGAGCCCGACTTTGGCCAGATC 1380
Qy 1381 CTGGAGGAGCTCGCTTACATTTCCCAATCGCTTCCGCTGCCAGAGAGAAAGCGAGCGT 1440
Db 1381 CTGGAGGAGCTCGCTTACATTTCCCAATCGCTTCCGCTGCCAGAGAGAGCGAGCGT 1440
Qy 1441 TGACGAGTGAAGTTCCCGCTGTGTGTGGACCGCTGTGCTCTATGGCTTCTCG 1500
Db 1441 TGACGAGTGAAGTTCCCGCTGTGTGTGGACCGCTGTGCTCTATGGCTTCTCG 1500
Qy 1501 GTCTTCAACCATCATCTGCAACCATCGCATCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
Db 1501 GTCTTCAACCATCATCTGCAACCATCGCATCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
Qy 1561 GTGTCCAAAGACTTTTGGCTAAGCAACCGCTTCTGTATCATGTGGAATACTCACAGATG 1620
Db 1561 GTGTCCAAAGACTTTTGGCTAAGCAACCGCTTCTGTATCATGTGGAATACTCACAGATG 1620
Qy 1621 GCAAGCGCTTGGCTTGGCGAGATTTGGGGGTGCTAATCCAGACAGCATTAACGCCAC 1680
Db 1621 GCAAGCGCTTGGCTTGGCGAGATTTGGGGGTGCTAATCCAGACAGCATTAACGCCAC 1680
Qy 1681 AACTCCAGTGTCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
Db 1681 AACTCCAGTGTCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
Qy 1741 GTAGTAGAATCTCAGACATTTGTTTCAATCTCAGATGGCTGATAGATATCTTTGGCA 1800
Db 1741 GTAGTAGAATCTCAGACATTTGTTTCAATCTCAGATGGCTGATAGATATCTTTGGCA 1800
Qy 1801 CATCCGTACATCGGTGAGCGGCACTGAGTGTGATTTGCTGCTGCTGCTGCTGCTGCTGCT 1860
Db 1801 CATCCGTACATCGGTGAGCGGCACTGAGTGTGATTTGCTGCTGCTGCTGCTGCTGCTGCT 1860
Qy 1861 TGGAAAGCCCTTCGGA 1876
Db 1861 TGGAAAGCCCTTCGGA 1876

RESULT 5

ADAL0864

ID ADAL0864 standard; DNA; 1376 BP.

AC ADAL0864;

XX XX

DT 06-NOV-2003 (first entry)

XX XX

DE Human neuronal nicotinic acetylcholine receptor alpha 7 subunit DNA.

XX XX

KW db; gene; alpha 7 subunit; human;

KW neuronal nicotinic acetylcholine receptor; ligand-gated ion channel;

KW synaptic transmission; gene therapy; transgenic.

XX XX

OS Homo sapiens.

XX XX

FH Key Location/Qualifiers

FT 5'UTR 1..72

FT FT /*tag= a

FT CDS 73..1584

FT FT /*tag= b

FT FT /product= "nAChR alpha 7 subunit"

FT FT

FT	3'UTR	1585..1876	
FT		/*tag= c	
XX			
PN	US6524789-B1.		
XX			
PD	25-FEB-2003.		
XX			
PF	07-JUN-1996;	96US-00660451.	
XX			
PR	07-JUN-1995;	95US-00484722.	
XX			
PA	(MERI) MERCK & CO INC.		
XX			
PI	Elliott KJ, Harpold WM;		
DR	WPI; 2003-511917/48.		
DR	P-PSDB; ADA10874.		
XX			
PT	New nucleic acid encoding an alpha-6 or a beta-3 subunit of a human		
PT	neuronal nicotinic acetylcholine receptor (nAChR), useful for identifying		
PT	compounds that modulate human neuronal nAChR activity.		
XX			
PS	Claim 33; Col 67-72; 63pp; English.		
XX			
CC	The invention relates to an isolated nucleic acid molecule comprising a		
CC	nucleotide sequence encoding an alpha 6 or a beta 3 subunit of a human		
CC	neuronal nicotinic acetylcholine receptor nAChR. nAChR's form ligand-		
CC	gated ion channels that mediate synaptic transmissions between nerve and		
CC	muscle and between neurons upon interaction with the neurotransmitter		
CC	acetylcholine. The nucleic acid molecule is useful for identifying		
CC	compounds that modulate human neuronal nAChR. The present sequence		
CC	represents DNA encoding the human neuronal nicotinic acetylcholine		
CC	receptor, nAChR, alpha 7 subunit. Note: the present sequence decodes to		
CC	the protein shown in ADA10874 not the one described in the specification		
CC	as being the nAChR alpha 7 subunit ADA10865.		
XX			
SQ	Sequence 1876 BP; 369 A; 553 C; 531 G; 423 T; 0 U; 0 Other;		
	Query Match	100.0%; Score 1875.6; DB 8; Length 1876;	
	Best Local Similarity	99.9%; Pred. No. 0;	
	Matches 1875; Conservative	1; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	GGCGCGAGCGCAGCGCCGGCGCAGACCGCAGAGCTGGAGCGCGCGCTCGCTGCAGCT	60
Db	1	GGCGCGAGCGCGCAGCGCCGGCGCAGACCGCAGAGCTGGAGCGCGCGCTCGCTGCAGCT	60
Qy	61	CCGGGACTCAACATGCGCTGCTCGCGGAGCGCTCTGCTGGCGCTGGCGCGCTCGCTC	120
Db	61	CCGGGACTCAACATGCGCTGCTCGCGGAGCGCTCTGCTGGCGCTGGCGCGCTCGCTC	120
Qy	121	CTGCACGCTGCTCCGCAAGGCGAGTTCAGAGGAAGCTTTTACAGAGAGCTGGTCAGAAC	180
Db	121	CTGCACGCTGCTCCGCAAGGCGAGTTCAGAGGAAGCTTTTACAGAGAGCTGGTCAGAAC	180
Qy	181	TACAATCCCTTGGAGAGCGCCGCTGCGCAATGACTCGCAACCACTCACCGTCTACTTCTCC	240
Db	181	TACAATCCCTTGGAGAGCGCCGCTGCGCAATGACTCGCAACCACTCACCGTCTACTTCTCC	240
Qy	241	CTGAGCCTCCTGCAGATCATGACGTGGATGAGAGAACCAAGTTTAAACCAACCAATT	300
Db	241	CTGAGCCTCCTGCAGATCATGACGTGGATGAGAGAACCAAGTTTAAACCAACCAATT	300
Qy	301	TGGCTGCAATGCTTTGACAGATCACTATTTTACAGTGGATGTCAGATATCCAGG	360
Db	301	TGGCTGCAATGCTTTGACAGATCACTATTTTACAGTGGATGTCAGATATCCAGG	360
Qy	361	GTGAAGACTGTTTCGTTTCCAGATGCCAGATTTGGAACACAGACATTTCTCTATTAAC	420
Db	361	GTGAAGACTGTTTCGTTTCCAGATGCCAGATTTGGAACACAGACATTTCTCTATTAAC	420
Qy	421	AGTGTGTATGAGCGCTTTGACGCCACATTTCCACACTTAACGTTTGGTGAATTTCTTGG	480
Db	421	AGTGTGTATGAGCGCTTTGACGCCACATTTCCACACTTAACGTTTGGTGAATTTCTTGG	480

QY 1561 GTGTCAAAGACATTTGGTAAACACAGCGCTGGTTCTGTACATGTGGAAACTCACAGATGG 1620
 Db 1561 GTGTCAAAGACATTTGGTAAACACAGCGCTGGTTCTGTACATGTGGAAACTCACAGATGG 1620
 QY 1621 GCAAGGCTTTGGCTTGGCGAGATTTGGGGTGTCTAATCCAGGACAGCATTAACGCCAC 1680
 Db 1621 GCAAGGCTTTGGCTTGGCGAGATTTGGGGTGTCTAATCCAGGACAGCATTAACGCCAC 1680
 QY 1681 AACTCCAGTGTTCCTTCTGGCTGTACAGTCTGTGTGTCTTACGGTTCTTTGTTACTTTAG 1740
 Db 1681 AACTCCAGTGTTCCTTCTGGCTGTACAGTCTGTGTGTCTTACGGTTCTTTGTTACTTTAG 1740
 QY 1741 GTAGTAGAATCTCAGCACTTTGTTTCTATATTTCTCAGATGGCGTGTATGATATCTTGGCA 1800
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 QY 1801 CATCCGTACCATCGGTCCAGCAGGCGCACTGAGTAGTCAATTTGCGCATTAAGCCACTGCC 1860
 Db 1801 CATCCGTACCATCGGTCCAGCAGGCGCACTGAGTAGTCAATTTGCGCATTAAGCCACTGCC 1860
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 Db 1861 TGGAAAGCCCTTCGGA 1876
 RESULT 6
 ABZ11298
 ID ABZ11298 standard; cDNA; 1964 BP.
 XX
 AC ABZ11298;
 XX
 DT 20-JAN-2003 (first entry)
 XX
 DE Human polynucleotide SEQ ID NO 180.
 XX
 KW Human; genome mapping; gene therapy; food supplement; virus; fungus;
 KW cell-proliferative disorder; neurodegenerative disease; bacterial;
 KW Parkinson's disease; Alzheimer's disease; autoimmune disease;
 KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
 KW arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;
 KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
 KW haemostatic; vulnery; fungicide; antibacterial; virucide; protozoicide;
 KW antiarthritic; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200270539-A2.
 XX
 PD 12-SEP-2002.
 XX
 PF 05-MAR-2002; 2002WO-US005095.
 XX
 PR 05-MAR-2001; 2001US-00799451.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
 PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
 PI Wehrman T, Wang J, Wang D, Drmanac RT;
 XX
 DR WPI; 2002-759812/82.
 DR P-FSDB; ABP69081.
 XX
 PT New polynucleotides comprising sequences assembled from expressed
 PT sequence tags (ESTs), useful for treating cell-proliferative,
 PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
 PT or coagulation disorders.
 XX
 PS Claim 1; SEQ ID NO 180; 1012pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated polynucleotide (I) comprising a
 CC nucleotide sequence selected from any of 948 sequences (ABZ11119-
 CC ABZ12066) or their mature protein coding portion, active domain coding

CC protein or complementary sequences. The polynucleotides are useful for
 CC identifying expressed genes or for physical mapping of human genome. The
 CC encoded polypeptides (ABP6902-ABP6949) are useful as molecular weight
 CC markers, as a food supplement, for generating antibodies, in medical
 CC imaging, screening and diagnostic assays and for treating cell-
 CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
 CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
 CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
 CC platelet or coagulation disorders, wound, burns, fungal, parasitic,
 CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
 CC arthritis, etc. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pat_sequences
 XX
 XX Sequence 1964 BP; 415 A; 567 C; 523 G; 459 T; 0 U; 0 Other;
 Query Match 95.1%; Score 1787; DB 6; Length 1964;
 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 1802; Conservative 1; Mismatches 6; Indels 2; Gaps 1;
 QY 66 ACTCAACATGCGCTGTCTGCGCGGAGCGGTCTGGCTGGCGCTGGCGCGTGGCTGGCA 125
 Db 1 ACTCAACATGCGCTGTCTGCGCGGAGCGGTCTGGCTGGCGCTGGCGCGTGGCTGGCA 60
 QY 126 CGTGTCCCTGCAAGGCGAGTTCCAGAGGAGCTTTACAGGAGCTGGTCAAGAACTACAA 185
 Db 61 CGTGTCCCTGCAAGGCGAGTTCCAGAGGAGCTTTACAGGAGCTGGTCAAGAACTACAA 120
 QY 186 TCCCTTGGAGAGCGCGTGGCCCAATGACTCGCAACCACTCACCGTCTACTTCTCCCTGAG 245
 Db 121 TCCCTTGGAGAGCGCGTGGCCCAATGACTCGCAACCACTCACCGTCTACTTCTCCCTGAA 180
 QY 246 CTTCTGTCAGATCATGGAAGTGTGATGAGAAGAACCAAGTTTAAACCAACCACTTGGCT 305
 Db 181 CTTCTGTCAGATCATGGAAGTGTGATGAGAAGAACCAAGTTTAAACCAACCACTTGGCT 240
 QY 306 GCAAAATGCTTGGACAGATCACTATTATACAGTGGAAATGTCTGAGATATCCAGGGTAA 365
 Db 241 GCAAAATGCTTGGACAGATCACTATTATACAGTGGAAATGTCTGAGATATCCAGGGTAA 300
 QY 366 GACTGTTCGTTTCCAGATGGCAGATTTGGAAACCAAGACATTTCTCTATACAGTGC 425
 Db 301 GACTGTTCGTTTCCAGATGGCAGATTTGGAAACCAAGACATTTCTCTATACAGTGC 360
 QY 426 TGATGAGCGCTTTGAGCGCCACATTTCCACATAGTGTGGTGAATTTCTTCTGGGCAATG 485
 Db 361 TGATGAGCGCTTTGAGCGCCACATTTCCACATAGTGTGGTGAATTTCTTCTGGGCAATG 420
 QY 486 CCAGTACCTGCCTCCAGGCATATTTCAAGAGTTCCTGTACATGATGATGCTGCTGTTTCC 545
 Db 421 CCAGTACCTGCCTCCAGGCATATTTCAAGAGTTCCTGTACATGATGATGCTGCTGTTTCC 480
 QY 546 CTTTGTATGTGAGCAGCTGCAAACTGAAAGTTTGGGTCTCTGTTCTTACGAGGCTGGTCTT 605
 Db 481 CTTTGTATGTGAGCAGCTGCAAACTGAAAGTTTGGGTCTCTGTTCTTACGAGGCTGGTCTT 538
 QY 606 GGATCTGCAGATGAGGAGGAGGAGTATCAAGTGTATATCCCAATGGAGAAATGGACCT 665
 Db 539 GGATCTGCAGATGAGGAGGAGGAGTATCAAGTGTATATCCCAATGGAGAAATGGACCT 598
 QY 666 AGTGGGAATCCCGGCAAGAGAGGAGTGAAGGTTCTATGAGTGTCTGCAAGAGCGCTTACCC 725
 Db 599 AGTGGGAATCCCGGCAAGAGAGGAGTGAAGGTTCTATGAGTGTCTGCAAGAGCGCTTACCC 658
 QY 726 CGATGTGACCTTTCAGTGTGACCTGCGCCGAGAGAGCTTCTATGATGGCTTCAACCTGCT 785
 Db 659 TGATGTGACCTTTCAGTGTGACCTGCGCCGAGAGAGCTTCTATGATGGCTTCAACCTGCT 718
 QY 786 GATCCCTGTGTGTCTCATCTCCGCCCTCGCCCTGCTGTTCTGTTCTCTGCTGAGATTC 845
 Db 719 GATCCCTGTGTGTCTCATCTCCGCCCTCGCCCTGCTGTTCTGTTCTCTGCTGAGATTC 778
 QY 846 CGGGGAGAGAGATTTCCCTGGGGATAACAGTCTTACTCTCTTACCCTCTTTCATGCTGCT 905

Query Match 80.4%; Score 1508.6; DB 4; Length 1509;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1508; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 73 ATGCGCTCTCGCCGGAGGCGTCTGGCTGGCGCTGGCGGCTGCTCTCTGCACTGTC 132
Db 1 ATGCGCTCTCGCCGGAGGCGTCTGGCTGGCGCTGGCGGCTGCTCTCTGCACTGTC 60

QY 133 CTGCAAGCGAGTTCAGAGGAAGCTTTACAGAGAGCTGGTCAAGAACTTACAATCCCTTG 192
Db 61 CTGCAAGCGAGTTCAGAGGAAGCTTTACAGAGAGCTGGTCAAGAACTTACAATCCCTTG 120

QY 193 GAGAGCGCGTGGCCAAATGACTCGCAACCACTCAACCGTCTACTTCTCCCTGAGCCTCTG 252
Db 121 GAGAGCGCGTGGCCAAATGACTCGCAACCACTCAACCGTCTACTTCTCCCTGAGCCTCTG 180

QY 253 CAGATCATGAGCGTGGATGAGAGAACCAAGTCTTAAACCAACCAATTTGGTGCAGATG 312
Db 181 CAGATCATGAGCGTGGATGAGAGAACCAAGTCTTAAACCAACCAATTTGGTGCAGATG 240

QY 313 TCTTGGACAGATCACTATTATACAGTGGATGTGTGAGATATCCAGGGGTGAAGACTGT 372
Db 241 TCTTGGACAGATCACTATTATACAGTGGATGTGTGAGATATCCAGGGGTGAAGACTGT 300

QY 373 CGTTTCCAGATGGCCAGATTTGGAAACCAAGACATCTTCTATAACAGTGTCTGATGAG 432
Db 301 CGTTTCCAGATGGCCAGATTTGGAAACCAAGACATCTTCTATAACAGTGTCTGATGAG 360

QY 433 CGCTTTGAGCGCACATTCACACTAAGCTGTGGTGAATCTTCTGGGCTGAGCAGTAC 492
Db 361 CGCTTTGAGCGCACATTCACACTAAGCTGTGGTGAATCTTCTGGGCTGAGCAGTAC 420

QY 493 CTGCTCCAGGCATATTCAGAGTTCCTGCTACATCGATGTACGCTGGTTCCTTTCAT 552
Db 421 CTGCTCCAGGCATATTCAGAGTTCCTGCTACATCGATGTACGCTGGTTCCTTTCAT 480

QY 553 GTGAGCACTGCAAACTGAAGTTTGGTCTGCTGCTTACGAGGCTGCTCTGATGATCTG 612
Db 481 GTGAGCACTGCAAACTGAAGTTTGGTCTGCTGCTTACGAGGCTGCTCTGATGATCTG 540

QY 613 CAGATGAGGAGGAGATATCAGTGGCTATATCCCAATGGAGATGGACCTAGTGGGA 672
Db 541 CAGATGAGGAGGAGATATCAGTGGCTATATCCCAATGGAGATGGACCTAGTGGGA 600

QY 673 ATCCCGGCAAGAGAGTGAAGTTCATGAGTGTCTGCAAGAGCCCTACCCGATGTC 732
Db 601 ATCCCGGCAAGAGAGTGAAGTTCATGAGTGTCTGCAAGAGCCCTACCCGATGTC 660

QY 733 ACCTTCAAGTGAACCATGGCGGAGAGCTCTACTATGGCTCAACCTGCTGATCCCC 792
Db 661 ACCTTCAAGTGAACCATGGCGGAGAGCTCTACTATGGCTCAACCTGCTGATCCCC 720

QY 793 TGTGTGCTCATCTCGCCCTGSCCTGCTGGTGTCTCTGCTGAGATTCGGGGAG 852
Db 721 TGTGTGCTCATCTCGCCCTGSCCTGCTGGTGTCTCTGCTGAGATTCGGGGAG 780

QY 853 AAGATTTCCCTGGGATAACAGTCTTACTCTCTTACCGTCTTATGCTGCTGCTGGT 912
Db 781 AAGATTTCCCTGGGATAACAGTCTTACTCTCTTACCGTCTTATGCTGCTGCTGGT 840

QY 913 GAGATCATGCGCAACATCCGATTCGGTACCATTTGATAGCCAGTACTTCCGCGAGCC 972
Db 841 GAGATCATGCGCGCAACATCCGATTCGGTACCATTTGATAGCCAGTACTTCCGCGAGCC 900

QY 973 ATGATCATGCGGCTCTCGGTGGTGGAGGCTGATGCTGCTGAGTACCAACCAACC 1032
Db 901 ATGATCATGCGGCTCTCGGTGGTGGAGGCTGATGCTGCTGAGTACCAACCAACC 960

QY 1033 GACCCCGAGCGGGCAAGATGCCCAAGTGGACAGAGTCACTCTTCTGAACCTGGTGGG 1092
Db 961 GACCCCGAGCGGGCAAGATGCCCAAGTGGACAGAGTCACTCTTCTGAACCTGGTGGG 1020

QY 1093 TGGTTCCTSCAATGAAG 1152
Db 1021 TGGTTCCTSCAATGAAG 1080

QY 1153 CAGCGGCGCTCAGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1212
Db 1081 CAGCGGCGCTCAGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140

QY 1213 AACGGGAACCTGCTGTATCATCGGCTTCGCGGCTTCGAGCGGCTGCACTGTGTCCGAGC 1272
Db 1141 AACGGGAACCTGCTGTATCATCGGCTTCGCGGCTTCGAGCGGCTGCACTGTGTCCGAGC 1200

QY 1273 CCGGAGCTGCGGCTGAGTGTGTGGCGGATGTGTCTCCCAACGCAAGATGAGCACTTC 1332
Db 1201 CCGGAGCTGCGGCTGAGTGTGTGGCGGATGTGTCTCCCAACGCAAGATGAGCACTTC 1260

QY 1333 CTGCAAGCGGCGAG 1392
Db 1261 CTGCAAGCGGCGAG 1320

QY 1393 CGCTACATTTGCAATTCGCTTCGCTGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 1452
Db 1321 CGCTACATTTGCAATTCGCTTCGCTGCTGCGAGAGAGAGAGAGAGAGAGAGAG 1380

QY 1453 AAGTTGCGCGCTGAGTGTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1512
Db 1381 AAGTTGCGCGCTGAGTGTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440

QY 1513 ATCTGCACCATTCGAGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1572
Db 1441 ATCTGCACCATTCGAGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500

QY 1573 TTTGCGTAA 1581
Db 1501 TTTGCGTAA 1509

RESULT 9
AAC90385
ID AAC90385 standard; cDNA; 1509 BP.
XX
AC AAC90385;
XX
DT 14-MAR-2001 (first entry)
XX
DE Mutant human alpha7 ligand gated ion channel coding sequence #1.
XX
KW Human; alpha7 nicotinic acetylcholine gated ion channel; mutant;
KW 5-hydroxytryptamine; 5-HT3; calcium ion conductance; ss.
XX
OS Homo sapiens.
XX
PN WO200073431-A2.
XX
PD 07-DEC-2000.
XX
PF 25-MAY-2000; 2000WO-US011862.
XX
PR 27-MAY-1999; 99US-0136174P.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
XX Groppi VE, Wolfe ML, Berkenpas MB;
XX
XX WPI; 2001-061524/07.
XX
XX P-PSDB; AAB50015.
XX
XX Special cell culture medium for treating cells and for inducing mammalian
XX cell lines to conduct calcium ions, comprising specified concentrations
XX of ions of sodium, calcium and potassium at specified pH.
XX
XX Claim 50; Page 69; 77pp; English.

PI Groppi VE, Wolfe ML, Berkenpas MB;
XX WPI; 2001-061524/07.
DR P-PSDB; AAB50016.
XX
XX Special cell culture medium for treating cells and for inducing mammalian
PT cell lines to conduct calcium ions, comprising specified concentrations
PT of ions of sodium, calcium and potassium at specified pH.
XX
XX Claim 57; Page 72; 77pp; English.
XX
XX The present sequence is the coding sequence for a mutant human alpha7
CC nicotinic acetylcholine gated ion channel. The human alpha7 ion channel
CC was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3)
CC chimeric ligand gated ion channel (see AAC90382 and AAB50014). The
CC alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells
CC in the present invention, resulting in preferential calcium ion
CC conductance by the cells. The protein encoded by this sequence has the
CC wild-type cysteine residue at position 241 substituted by a serine
CC residue
XX
SQ Sequence 1509 BP; 298 A; 451 C; 429 G; 331 T; 0 U; 0 Other;
Query Match 80.3%; Score 1507; DB 4; Length 1509;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1507; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 73 ATGCGCTCTCGCGGGAGGCGTCTGGCTGGCGCTGGCGGCTCTCTGCAAGTGTCC 132
DB 1 ATGCGCTCTCGCGGGAGGCGTCTGGCTGGCGCTGGCGGCTCTCTGCAAGTGTCC 60
QY 133 CTGCAAGCGGAGTTCAGAGGAGCTTTTCAAGAGCTGGTCAAGACTCAATCCCTTG 192
DB 61 CTGCAAGCGGAGTTCAGAGGAGCTTTTCAAGAGCTGGTCAAGACTCAATCCCTTG 120
QY 193 GAGAGGCGCTGGCGCAATGACTCGCAACACTCACCGTCTACTTCTCCCTGAGCCTCCTG 252
DB 121 GAGAGGCGCTGGCGCAATGACTCGCAACACTCACCGTCTACTTCTCCCTGAGCCTCCTG 180
QY 253 CAGATCATGGAGCTGGAGTGAAGAACCAAGTTTAAACCAACCAATTTGGCTGCAATG 312
DB 181 CAGATCATGGAGCTGGAGTGAAGAACCAAGTTTAAACCAACCAATTTGGCTGCAATG 240
QY 313 TCTTGGACAGATCACTATTTCAGTGGATGTGTGAGATATTCAGGAGTGAAGTGT 372
DB 241 TCTTGGACAGATCACTATTTCAGTGGATGTGTGAGATATTCAGGAGTGAAGTGT 300
QY 373 CGTTTCCAGATGGCGAGATTGGAAACAGACATCTTCTCTATAACAGTGTGATGAG 432
DB 301 CGTTTCCAGATGGCGAGATTGGAAACAGACATCTTCTCTATAACAGTGTGATGAG 360
QY 433 CGTTTGGACGCAATTCACACTAACGTGTGGTGAATTTCTTGGGCAATGGCCAGTAC 492
DB 361 CGCTTTGACGCGCAATTCACACTAACGTGTGGTGAATTTCTTGGGCAATGGCCAGTAC 420
QY 493 CTGCTCCAGGCAATTCAGAGTTCCTGCTACATCGATGATGAGTGTTCCTTTCAT 552
DB 421 CTGCTCCAGGCAATTCAGAGTTCCTGCTACATCGATGATGAGTGTTCCTTTCAT 480
QY 553 GTGACGACTGCAAACTGAAGTTTGGGTCCTGGTCTTACGAGGCTGGTCTTGGATCTG 612
DB 481 GTGACGACTGCAAACTGAAGTTTGGGTCCTGGTCTTACGAGGCTGGTCTTGGATCTG 540
QY 613 CAGATGCAAGGAGGAGATATCAGTGGCTATATCCCAATGGAGAAATAGTGGGA 672
DB 541 CAGATGCAAGGAGGAGATATCAGTGGCTATATCCCAATGGAGAAATAGTGGGA 600
QY 673 ATCCCGGCAAGAGAGTGAAGTTTCTATGAGTGTCTGCAAGAGCCCTACCCGATGTC 732
DB 601 ATCCCGGCAAGAGAGTGAAGTTTCTATGAGTGTCTGCAAGAGCCCTACCCGATGTC 660
QY 733 ACCTTCAAGTGAACATCGCGCGAGGAGCTCTACTATGGCTCAACTGCTGATCCCG 792

DB 661 ACCTTCAAGTGAACCATGCGCCGAGGAGCGCTTACTATAGCCCTCAACCTGCTGATCCCC 720
QY 793 TGTGTGCTCATCTCCGCCCTCGCCCTGCTGTGTGTTCTGTCTTCTGAGATTTCGGGGAG 852
DB 721 AGTGTGCTCATCTCCGCCCTCGCCCTGCTGTGTGTTCTGTCTTCTGAGATTTCGGGGAG 780
QY 853 AAGATTTCCTCGGGGATAAAGTCTTACTCTCTTCTTACCGTCTTCACTGCTGCTGCTGCT 912
DB 781 AAGATTTCCTCGGGGATAAAGTCTTACTCTCTCTTACCGTCTTCACTGCTGCTGCTGCT 840
QY 913 GAGATCATGCGCGCAACATCCGATTTCGGTACCATTTAGTACCCAGTACTTCCGCCAGCACC 972
DB 841 GAGATCATGCGCGCAACATCCGATTTCGGTACCATTTAGTACCCAGTACTTCCGCCAGCACC 900
QY 973 ATGATCATGCTGGGCTCTCGGTGGTGTGAGGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1032
DB 901 ATGATCATGCTGGGCTCTCGGTGGTGTGAGGCTGTGCTGTGCTGTGCTGTGCTGTGCT 960
QY 1033 GACCCGAGCGGGGCAAGATGCCCCAAGTGGACCAAGTGTGCTGTGCTGTGCTGTGCTGTGCT 1092
DB 961 GACCCGAGCGGGGCAAGATGCCCCAAGTGGACCAAGTGTGCTGTGCTGTGCTGTGCTGTGCT 1020
QY 1093 TGGTTCCTTCGAATGAAGAGCGCGGGGAGGACAAGTGTGCGCGCTGCGCCAGCACAAG 1152
DB 1021 TGGTTCCTTCGAATGAAGAGCGCGGGGAGGACAAGTGTGCGCGCTGCGCCAGCACAAG 1080
QY 1153 CAGCGGCGCTGCACGCTGGCAGTGTGAGATGAGCGCGGTGGCGCGCGCGCGCGCGCGC 1212
DB 1081 CAGCGGCGCTGCACGCTGGCAGTGTGAGATGAGCGCGGTGGCGCGCGCGCGCGCGCGC 1140
QY 1213 AACGGGAACCTGCTGTATCATCGGCTTCGGCGGCTGTGACGCGCGTGTGCTGTGCTGTGCT 1272
DB 1141 AACGGGAACCTGCTGTATCATCGGCTTCGGCGGCTGTGACGCGCGTGTGCTGTGCTGTGCT 1200
QY 1273 CCCGACTCTGGGCTAGTGTGGCGCATGTCCTGCTCCCGCAGCAGATGAGCAGCTC 1332
DB 1201 CCCGACTCTGGGCTAGTGTGGCGCATGTCCTGCTCCCGCAGCAGATGAGCAGCTC 1260
QY 1333 CTGCAACGCGGCAACCCCGAGGGGACCCCGGACTTTGGCAAGATCTCTGGAGAGGTC 1392
DB 1261 CTGCAACGCGGCAACCCCGAGGGGACCCCGGACTTTGGCAAGATCTCTGGAGAGGTC 1320
QY 1393 CGCTACATGTCATTCGTTCCGCTGCGAGCAAGAGCGAGGCGGTCTGAGCGAGTGG 1452
DB 1321 CGCTACATGTCATTCGTTCCGCTGCGAGCAAGAGCGAGGCGGTCTGAGCGAGTGG 1380
QY 1453 AAGTTTCGCGGCTGTGTGTGACCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1512
DB 1381 AAGTTTCGCGGCTGTGTGTGACCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1440
QY 1513 ATCTGACCAATCGGCTATCTGATTCGCTCCCAACTTCTGAGAGGCGGTGTCCAAAGAC 1572
DB 1441 ATCTGACCAATCGGCTATCTGATTCGCTCCCAACTTCTGAGAGGCGGTGTCCAAAGAC 1500
QY 1573 TTTTCGGTAA 1581
DB 1501 TTTTCGGTAA 1509
RESULT 11
AAC58395
ID AAC58395 standard; cDNA; 1509 BP.
XX AAC58395;
XX AC
XX AC
DT 29-JAN-2001 (first entry)
XX Human PRO2145 nucleotide sequence SEQ ID NO: 76.
DE Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
XX proliferation; tumorigenesis; identification; cancer; cytostatic;
KW neutrotic; neuroprotective; antiinflammatory; immunosuppressive;
KW immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;

KW neuronal disorder; glial disorder; astrocytal disorder; angiogenic;
 KW hypothalamic disorder; glandular disorder; macrophagal disorder;
 KW epithelial disorder; stromal disorder; blastocoeic disorder;
 KW inflammatory disorder; immunologic disorder; ss.

XX Homo sapiens.

PN WO200053755-A2.

XX 14-SEP-2000.

PF 06-JAN-2000; 2000WO-US000376.

XX 08-MAR-1999; 99WO-US005028.

PR 02-JUN-1999; 99WO-US012252.

PR 23-JUN-1999; 99US-0141037P.

PR 07-JUL-1999; 99US-0143048P.

PR 26-JUL-1999; 99US-0145698P.

PR 30-NOV-1999; 99WO-US028313.

PR 20-DEC-1999; 99WO-US030911.

PR 05-JAN-2000; 2000WO-US000219.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;
 PI Watanabe CK, Wood WI;

XX WPI; 2000-572270/53.

DR P-PSDB; AAB24088.

XX Thirty PRO polynucleotides encoding PRO polypeptides, useful in the

PT treatment, diagnosis and prevention of cancer.

XX Claim 50; Fig 57; 286pp; English.

XX The present invention describes an isolated antibody that binds to one of

CC the human PRO proteins designated PRO212, PRO290, PRO341, PRO335, PRO619,

CC PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009, PRO1025,

CC PRO1030, PRO1097, PRO1153, PRO1182, PRO1184, PRO1187,

CC PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094, PRO2145 OR

CC PRO2198. PRO antagonists can be used to inhibit tumour cell growth. The

CC PRO polypeptides and nucleotides are useful in the treatment, diagnosis

CC and prevention of cancer. The antibodies and other anti-tumour compounds

CC maybe used to treat various conditions, including those characterised by

CC overexpression and/or activation of the amplified PRO genes. Exemplary

CC conditions or disorders to be treated with such antibodies and other

CC compounds include benign or malignant tumours (e.g., renal, liver,

CC kidney, bladder, breast, gastric, ovarian, colorectal, prostate,

CC pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas,

CC glioblastomas, and various head and neck tumours), leukaemias and

CC lymphoid malignancies, other disorders such as neuronal, glial,

CC astrocytal, hypothalamic and other glandular, macrophagal, epithelial,

CC stromal and blastocoeic disorders, and inflammatory, angiogenic and

CC immunologic disorders. AAC58242 to AAC58366 represent PCR primers and

CC hybridisation probes used in the isolation of the human PRO sequences.

CC AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human PRO

CC polynucleotide and protein sequences given in the exemplification of the

CC present invention

XX Sequence 1509 BP; 297 A; 451 C; 429 G; 332 T; 0 U; 0 Other;

SQ

Query Match 80.2%; Score 1505.4; DB 3; Length 1509;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1506; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 73 ATGGCTGCTCGCCGGGAGGCGTCTGGCTGGCGTGGCGCGTGGCTGCTGCGACGTGTC 132

1 ATGGCTGCTCGCCGGGAGGCGTCTGGCTGGCGTGGCGCGTGGCTGCTGCGACGTGTC 60

133 CTGCAAGCGGAGTTCCAGAGAAAGCTTTACAGAGAGTGGTTCAGAACTACAATCCCTTG 192

61 CTGCAAGCGGAGTTCCAGAGAAAGCTTTACAGAGAGTGGTTCAGAACTACAATCCCTTG 120

Qy 193 GAGAGCCCGTGGCCAAATGACTCGCAACCACTCACCGTCTACTTCTCCCTGAGCCTCCG 252
 Db 121 GAGAGCCCGTGGCCAAATGACTCGCAACCACTCACCGTCTACTTCTCCCTGAGCCTCCG 180
 Qy 253 CAGATCATGGAGCGTGGATGAGNAGAACCAAGTTTTAAACCAACCAATTTGGCTGCAAAATG 312
 Db 181 CAGATCATGGAGCGTGGATGAGNAGAACCAAGTTTTAAACCAACCAATTTGGCTGCAAAATG 240
 Qy 313 TCTTGGACAGATCACTATTTTACAGTGGAAATGTGTGAGAAATATCCAGGGGTGAAGACTGTT 372
 Db 241 TCTTGGACAGATCACTATTTTACAGTGGAAATGTGTGAGAAATATCCAGGGGTGAAGACTGTT 300
 Qy 373 CGTTTCCAGATGGCCAGATTTGGAAAACAGACATTTCTTCTATAACAGTCTGATGAG 432
 Db 301 CGTTTCCAGATGGCCAGATTTGGAAAACAGACATTTCTTCTATAACAGTCTGATGAG 360
 Qy 433 CGCTTTGAGCCACATTTCCACACTAACGTTGGTGAATTTCTTCTGGGCAATTCACAGTAC 492
 Db 361 CGCTTTGAGCCACATTTCCACACTAACGTTGGTGAATTTCTTCTGGGCAATTCACAGTAC 420
 Qy 493 CTGCTCCAGGCAATTTCAAGAGTTCTCTGCTACATCGATGTACGCTGGTTTCCCTTTGAT 552
 Db 421 CTGCTCCAGGCAATTTCAAGAGTTCTCTGCTACATCGATGTACGCTGGTTTCCCTTTGAT 480
 Qy 553 GTGAGCACTGCAAACTGAAGTTGGTCTCTTACGAGGCTGCTCTTGGATCTG 612
 Db 481 GTGAGCACTGCAAACTGAAGTTGGTCTCTTACGAGGCTGCTCTTGGATCTG 540
 Qy 613 CAGATGAGGAGGAGATATCAGTGGCTATATCCCCAATGGAGAAATGGGACCTAGTGGGA 672
 Db 541 CAGATGAGGAGGAGATATCAGTGGCTATATCCCCAATGGAGAAATGGGACCTAGTGGGA 600
 Qy 673 ATCCCGGCAAGAGGAGTGAAGGTTCTATGATGTCTGCAAGAGCCCTACCCCGATGTC 732
 Db 601 ATCCCGGCAAGAGGAGTGAAGGTTCTATGATGTCTGCAAGAGCCCTACCCCGATGTC 660
 Qy 733 ACCTTCAGATGACCAATCGCCGAGGAGCTCTACTATGGGCTCAACTGCTGATCCCC 792
 Db 661 ACCTTCAGATGACCAATCGCCGAGGAGCTCTACTATGGGCTCAACTGCTGATCCCC 720
 Qy 793 TGTGTCTCATCTCCGCCCTCGCCCTGCTGGTGTCTCTCTTCTCTGAGATTCGCGGAG 852
 Db 721 TGTGTCTCATCTCCGCCCTCGCCCTGCTGGTGTCTCTCTTCTCTGAGATTCGCGGAG 780
 Qy 853 AGATTTTCCCTGGGAGTAAACAGTTTACTTCTCTTCTTACCGTCTTATGCTGCTGCTG 912
 Db 781 AAGATTTCCCTGGGAGTAAACAGTTTACTTCTCTTCTTACCGTCTTCTGCTGCTGCTG 840
 Qy 913 GAGATCATGCCGCAACATCCGATTCGGTACCATTCATAGCCAGTACTTTCGCGACACC 972
 Db 841 GAGATCATGCCGCAACATCCGATTCGGTACCATTCATAGCCAGTACTTTCGCGACACC 900
 Qy 973 ATGATCATCGTGGGCTCTCGGTGGTGGTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1032
 Db 901 ATGATCATCGTGGGCTCTCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 960
 Qy 1033 GACCCGAGCGGGGCAAGATGCCAAGTGGACAGAGTCAATCTTCTGAACTGGTGGCG 1092
 Db 961 GACCCGAGCGGGGCAAGATGCCAAGTGGACAGAGTCAATCTTCTGAACTGGTGGCG 1020
 Qy 1093 TGGTTCTCTSCGAATGAAGAGGCCCGGGGAGGACCAAGTGGCGCCGCTGCGCAGCAACAG 1152
 Db 1021 TGGTTCTCTSCGAATGAAGAGGCCCGGGGAGGACCAAGTGGCGCCGCTGCGCAGCAACAG 1080
 Qy 1153 CAGCGGCGTGCAGCCTGGCCAGTGTGGAGATGAGCCCGTGGCGCGCGCGCGCGCGCAGC 1212
 Db 1081 CAGCGGCGTGCAGCCTGGCCAGTGTGGAGATGAGCGCGTGGCGCGCGCGCGCGCGCAGC 1140
 Qy 1213 AACGGAACTGTGTGTACATGGCTTCGCGGCGCTTGGAGCGGCTGCACTGTGTCCCGACC 1272
 Db 1141 AACGGAACTGTGTGTACATGGCTTCGCGGCGCTTGGAGCGGCTGCACTGTGTCCCGACC 1200
 Qy 1273 CCCGACTCTGGGAGTGTGTGTGGCGCATGGCGCTGCTCCCCCAGCAGCATGAGCACCTC 1332

Db 1201 CCCGACTCTGGGGTAGTGTGTGGCGCATGTCCTCCGCCACGACGATGAGCACTC 1260
Qy 1333 CTGCAAGCGGGCAACCCCGAGGGGACCCGGACTTTGGCCAAAGATCCTCGAGGAGGTC 1392
Db 1261 CTGCAAGCGGGCAACCCCGAGGGGACCCGGACTTTGGCCAAAGATCCTCGAGGAGGTC 1320
Qy 1393 CGCTACATTGCCAATCGCTTCCGCTGCGCAGGACGAAAGCGAGGGGCTGCGAGCGAGTGG 1452
Db 1321 CGCTACATTGCCAATCGCTTCCGCTGCGCAGGACGAAAGCGAGGGGCTGCGAGCGAGTGG 1380
Qy 1453 AAGTTCGCGGCTGTGTGGTGGACCGGCTGTGCTCATGGCTTCTCGGTTCTTCAACATC 1512
Db 1381 AAGTTCGCGGCTGTGTGGTGGACCGGCTGTGCTCATGGCTTCTCGGTTCTTCAACATC 1440
Qy 1513 ATCTGCAACCATCGGCATCTCTGATGTCGGCTCCCAACTTCGTGGAGGCGGTGTCCAAAGAC 1572
Db 1441 ATCTGCAACCATCGGCATCTCTGATGTCGGCTCCCAACTTCGTGGAGGCGGTGTCCAAAGAC 1500
Qy 1573 TTTGCGTAA 1581
Db 1501 TTTGCGTAA 1509

RESULT 12

AAC90387
ID AAC90387 standard; cDNA; 1509 BP.

XX AAC90387;

XX AC
XX DT
XX 14-MAR-2001 (first entry)

XX Mutant human alpha7 ligand gated ion channel coding sequence #3.

XX Human; alpha7 nicotinic acetylcholine gated ion channel; mutant;
XX 5-hydroxytryptamine; 5-HT3; calcium ion conductance; ss.

XX Homo sapiens.

XX WO200073431-A2.

XX 07-DEC-2000.

XX 25-MAY-2000; 2000WO-US011862.

XX 27-MAY-1999; 99US-0136174P.

XX (PHAA) PHARMACIA & UPJOHN CO.

XX Groppi VE, Wolfe ML, Berkenpas MB;

XX WPI; 2001-061524/07.

XX P-PSDB; AAB50017.

XX Special cell culture medium for treating cells and for inducing mammalian
XX cell lines to conduct calcium ions, comprising specified concentrations
XX of ions of sodium, calcium and potassium at specified pH.

XX Claim 64; Page 75; 77pp; English.

XX The present sequence is the coding sequence for a mutant human alpha7
XX nicotinic acetylcholine gated ion channel. The human alpha7 ion channel
XX was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3)
XX chimeric ligand gated ion channel (see AAC90382 and AAB50014). The
XX alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells
XX in the present invention, resulting in preferential calcium ion
XX conductance by the cells. The protein encoded by this sequence has the
XX wild-type threonine residue at position 230 substituted by a proline
XX residue and the wild-type cysteine residue at position 241 substituted by
XX a serine residue

XX Sequence 1509 BP; 297 A; 452 C; 429 G; 331 T; 0 U; 0 Other;

Query Match 80.2%; Score 1505.4; DB 4; Length 1509;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1506; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 73 ATGGGCTGCTGCGCGGAGGCGTCTGGCTGGCGCTGGCGGCTGCTCTGCAAGTGTCC 132
Db 1 ATGCGCTGCTGCGCGGAGGCGTCTGGCTGGCGCTGGCGGCTGCTCTGCAAGTGTCC 60
Qy 133 CTGCAAGCGGAGTTCAGAGGAGAGCTTTTACAAGGAGCTGGTCAAGAACTACAATCCCTTG 192
Db 61 CTGCAAGCGGAGTTCAGAGGAGAGCTTTTACAAGGAGCTGGTCAAGAACTACAATCCCTTG 120
Qy 193 GAGAGGCCCTGGCCAAATGACTCGCAACCACTCAACCGTCTACTTCTCCCTGAGGCTCTG 252
Db 121 GAGAGGCCCTGGCCAAATGACTCGCAACCACTCAACCGTCTACTTCTCCCTGAGGCTCTG 180
Qy 253 CAGATCATGAGCGGTGATGAGAGAACCAAGTTTAAACCAACCAATTTGGCTGCAATG 312
Db 181 CAGATCATGAGCGGTGATGAGAGAACCAAGTTTAAACCAACCAATTTGGCTGCAATG 240
Qy 313 TCTTGACAGATCACTATTTTACAGTGAATGTGTCAAGATATCCAGGGGTGAAGACTGTT 372
Db 241 TCTTGACAGATCACTATTTTACAGTGAATGTGTCAAGATATCCAGGGGTGAAGACTGTT 300
Qy 373 CGTTTCCAGATGCCAGATTTGGAACCAAGACATCTTCTCTATAACAGTGTGTGATGAG 432
Db 301 CGTTTCCAGATGCCAGATTTGGAACCAAGACATCTTCTCTATAACAGTGTGTGATGAG 360
Qy 433 CGCTTTGACGCCCATTTCCACACTTAACGCTGTGGTGAATTTCTTCTGGGCAATGCGAGTAC 492
Db 361 CGCTTTGACGCCCATTTCCACACTTAACGCTGTGGTGAATTTCTTCTGGGCAATGCGAGTAC 420
Qy 493 CTGCTCTCAGGCGATATTTCAAGAGTTCCTGCTACATCGATGTACGCTGGTTTCCCTTTGAT 552
Db 421 CTGCTCTCAGGCGATATTTCAAGAGTTCCTGCTACATCGATGTACGCTGGTTTCCCTTTGAT 480
Qy 553 GTGCAAGCTGCAAACTGAAGTTTGGTCTCTGCTTTACGAGGCTGGTCTTGGATCTG 612
Db 481 GTGCAAGCTGCAAACTGAAGTTTGGTCTCTGCTTTACGAGGCTGGTCTTGGATCTG 540
Qy 613 CAGATGAGGAGGAGCAGATATCAGTGGCTATATCCCAATGAGAACTGGACCTAGTGGGA 672
Db 541 CAGATGAGGAGGAGCAGATATCAGTGGCTATATCCCAATGAGAACTGGACCTAGTGGGA 600
Qy 673 ATCCCGGCAAGAGGAGTGAAGTTTCTATGAGTGTCTGCAAGAGCCCTACCCCGATGTC 732
Db 601 ATCCCGGCAAGAGGAGTGAAGTTTCTATGAGTGTCTGCAAGAGCCCTACCCCGATGTC 660
Qy 733 ACCTTCAAGTACCATGCGCGCAGGACGCTCTACTATGGCTCAACCTGCTGATCCCC 792
Db 661 ACCTTCAAGTACCATGCGCGCAGGACGCTCTACTATGGCTCAACCTGCTGATCCCC 720
Qy 793 TGTGTGCTCATCTCCGCCCTCGCCCTGCTGTGTCTCTCTGCTGAGATTTCCGGGAG 852
Db 721 AGTGTGCTCATCTCCGCCCTCGCCCTGCTGTGTCTCTCTGCTGAGATTTCCGGGAG 780
Qy 853 AAGATTTTCCCTGGGGATTAACAGTCTTACTCTCTTACCGCTTTTCATGCTGCTGCTGCT 912
Db 781 AAGATTTTCCCTGGGGATTAACAGTCTTACTCTCTTACCGCTTTTCATGCTGCTGCTGCT 840
Qy 913 GAGATCATGCGCGCAACATCGGATTCGGTACCATGTAGTACCCAGTACTTGGCCAGACC 972
Db 841 GAGATCATGCGCGCAACATCGGATTCGGTACCATGTAGTACCCAGTACTTGGCCAGACC 900
Qy 973 ATGATCATCTGGGCCCTCTCGGTGGTGTGACGCTGATCTGTGCTGAGTACCAACAC 1032
Db 901 ATGATCATCTGGGCCCTCTCGGTGGTGTGACGCTGATCTGTGCTGAGTACCAACAC 960
Qy 1033 GACCCCGAGCGGGCAAGATGCCCAAGTGGACAGAGTCACTCTTCTGAAGTGGTGGCG 1092
Db 961 GACCCCGAGCGGGCAAGATGCCCAAGTGGACAGAGTCACTCTTCTGAAGTGGTGGCG 1020
Qy 1093 TGGTTCTCTCGAATGAAGAGGCGCGGGGAGGAAGAAGTGGCGCGCGGCTGCGCACACAG 1152

Db 1021 TGGTTCCTCGCAATGAAGAGGCGCGGGAGGACAGAGTGCGCCGCTTGCAGCACAG 1080
Qy 1153 CAGCGCGCTGAGCTGAGCTGAGGAGAGGAGCGCGTGGCGCGCGCGCGCGCGCG 1212
Db 1081 CAGCGCGCTGAGCTGAGCTGAGGAGAGGAGCGCGTGGCGCGCGCGCGCGCGCG 1140
Qy 1213 AACGGGAACCTGCTGATACATCGCTTCCGCGGCTGGACGGGTGCACTGTGTCCGACC 1272
Db 1141 AACGGGAACCTGCTGATACATCGCTTCCGCGGCTGGACGGGTGCACTGTGTCCGACC 1200
Qy 1273 CCGGACTCTGGGAGTAGTGTGGCGCATGCTGCTCCCGACGACGACGACCTC 1332
Db 1201 CCGGACTCTGGGAGTAGTGTGGCGCATGCTGCTCCCGACGACGACGACCTC 1260
Qy 1333 CTGACGGCGGGCAACCCCGGAGGGGACCGGACTTGGCCAAAGATCTCGAGGAGGTC 1392
Db 1261 CTGACGGCGGGCAACCCCGGAGGGGACCGGACTTGGCCAAAGATCTCGAGGAGGTC 1320
Qy 1393 CGCTACATTGCCAATCGCTTCCGCTCCAGGACGAAAGCGAGCGGTCTGCAAGCGAGTGG 1452
Db 1321 CGCTACATTGCCAATCGCTTCCGCTCCAGGACGAAAGCGAGCGGTCTGCAAGCGAGTGG 1380
Qy 1453 AAGTTGCGCGCTGTGTGGTGGACCGCTGTGCTCATGGCTTCTCGGTCTTCACCATC 1512
Db 1381 AAGTTGCGCGCTGTGTGGTGGACCGCTGTGCTCATGGCTTCTCGGTCTTCACCATC 1440
Qy 1513 ATCTGACCATCGGATCTGATGTGCGGTCCCAACTTGTGGAGCGCGTGTCCAAAGAC 1572
Db 1441 ATCTGACCATCGGATCTGATGTGCGGTCCCAACTTGTGGAGCGCGTGTCCAAAGAC 1500
Qy 1573 TTTCGGTAA 1581
Db 1501 TTTCGGTAA 1509

RESULT 13

AAS79730
ID AAS79730 standard; cDNA; 2511 BP.
XX
AC AAS79730;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #15534.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
XX Homo sapiens.
XX
XX W0200175067-A2.
XX
XX 11-OCT-2001.
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XX 30-MAR-2001; 2001WO-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
XX 23-AUG-2000; 2000US-00649167.
XX
XX (HYSB-) HYSBQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX P-PSDB; ABG15543.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX
XX Claim 1; SEQ ID NO 15534; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 2511 BP; 523 A; 737 C; 692 G; 559 T; 0 U; 0 Other;
Query Match 68.2%; Score 1279; DB 5; Length 2511;
Best Local Similarity 98.6%; Pred. No. 1e-268;
Matches 1363; Conservative 1; Mismatches 11; Indels 8; Gaps 7;
Qy 500 CAGGCATATTCAGAGTTCTCTGCTACATCGATGATGCTTCCCTTTGATGTCAGC 559
Db 964 CAGGCATATTCAGAGTTCTCTGCTACATCGATGATGCTTCCCTTTGATGTCAGC 1023
Qy 560 ACTGCAAACTGAAGTTGGTCTCTTACGAGGCTGGTCTTGGATCTGCAATGC 619
Db 1024 ACTGCAAACTGAAGTTGGTCTCTTACGAGGCTGGTCTTGGATCTGCAATGC 1083
Qy 620 AGGA-GGCAAGATATC-AGTGGCTATATCCCAATGGAGATGGACCTAGTGGATCCC 677
Db 1084 AGGACGGCAGATATCAAGTGGCTATATCCCAATGGAGATGGACCTAGTGGATCCC 1143
Qy 678 CGGCAAGAGGAGTGAAAGTTCTTATGAGTGCTGCAAGAGCCCTACCCGATGTACCTT 737
Db 1144 CGGCAAGAGGAGTGAAAGTTCTTATGAGTGCTGCAAGAGCCCTACCTGATGTACCTT 1203
Qy 738 CACAGTGACCATCGCGCGCAGACGCTCTAATA--TGGCCTCAACCTGCTGATCCCTGT 795
Db 1204 CACAGTGACCATCGCGCGCAGACGCTCTAATAATGGGCTCAACCTGCTGATCCCTGT 1263
Qy 796 GTGCTCATCTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCT 854
Db 1264 GTGCTCATCTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCT 1323
Qy 855 GATTTCCCTCGGGATAACAGTCTTACTCTCTCTTACCTGCTTCTCATGCTGCTGCTGA 914
Db 1324 GATTTCCCTCGGGATAACAGTCTTACTCTCTCTTACCTGCTTCTCATGCTGCTGCTGA 1383
Qy 915 GATCATGCGCGCAACATCCGATTCGCTACATGATAGCCAGTACTTCCGACGACCAT 974
Db 1384 GATCATGCGCGCAACATCCGATTCGCTACATGATAGCCAGTACTTCCGACGACCAT 1443
Qy 975 GATCATGCGCGCTCTCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1034
Db 1444 GATCATGCGCGCTCTCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1503
Qy 1035 CCCCAGCGGGGCAAGATGCCCAAGTGACAGAGTCACTTCTTGAATGGTGGCGGTG 1094
Db 1504 CCCCAGCGGGGCAAGATGCCCAAGTGACAGAGTCACTTCTTGAATGGTGGCGGTG 1563
Qy 1095 GTTCTCTCGAATGAAGAGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1154
Db 1564 GTTCTCTCGAATGAAGAGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1623

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QY 1155 GCGCGCTGCAGCCTTGGCGCAGTGTGGAGATGAGCGCCGTGGCGCGCCGCGCCAGCAA 1214
Db 1624 GCGCGCTGCAGCCTTGGCGCAGTGTGGAGATGAGCGCCGTGGCGCGCCGCGCCAGCAA 1683
QY 1215 CGGNAACCTGTGTACATCGCTTCCGGCGCTTGGCGCGCTGACGCGGTGCACTGTGTCCGACCCC 1274
Db 1684 CGGNAACCTGTGTACATCGCTTCCGGCGCTTGGCGCGCTGACGCGGTGCACTGTGTCCGACCCC 1743
QY 1275 CGACTCTGGGTAGTGTGTGGCGCATGCGCTTCCCGCCAGCGAGCGCGCTTGGCGCGCTTCC 1334
Db 1744 CGACTCTGGGTAGTGTGTGGCGCATGCGCTTCCCGCCAGCGAGCGCGCTTGGCGCGCTTCC 1803
QY 1335 GCACGGCGGCAACCCCGCGAGGGGACCCCGACTTGGCCAAAGATCTTGGAGAGGTCGG 1394
Db 1804 GCACGGCGGCAACCCCGCGAGGGGACCCCGACTTGGCCAAAGATCTTGGAGAGGTCGG 1863
QY 1395 CTACATTGCCATCGCTTCCGCTGCGAGCGAGCGAGCGAGCGGTCTGCGAGGAGTGAA 1454
Db 1864 CTACATTGCCATCGCTTCCGCTGCGAGCGAGCGAGCGAGCGGTCTGCGAGGAGTGAA 1923
QY 1455 GTTCCGCGCTGTGTGTGGACCGGCTGTGCTCATGCGCTTCTCGGCTTCCACCATCAT 1514
Db 1924 GTTCCGCGCTGTGTGTGGACCGGCTGTGCTCATGCGCTTCTCGGCTTCCACCATCAT 1983
QY 1515 CTGACCAATCGGCACTCTGTATGTGGCTTCCCACTTCTGTGGAGCGCGTGTCCAAAGACTT 1574
Db 1984 CTGACCAATCGGCACTCTGTATGTGGCTTCCCACTTCTGTGGAGCGCGTGTCCAAAGACTT 2043
QY 1575 TGCGTAACCGCCTGTGTGTGTATGTGTGTAATGTGAAACTCACAGATGGGCAAGCCTTTGGC 1634
Db 2044 TGCGTAACCGC-ACTGTGTGTGTGTATGTGTGAAACTCACAGATGGGCAAGCCTTTGGC 2102
QY 1635 TTGCGGAGATTGGGGTGCTAATCCAGGACAGCAATTAACGCCCAACTCCAGGTGTCC 1694
Db 2103 TTGCGGAGATTGGGGTGCTAATCCAGGACAGCAATTAACGCCCAACTCCAGGTGTCC 2162
QY 1695 CTTCGCTGTACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1754
Db 2163 CTTCGCTGTACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2222
QY 1755 GCACCTTGTTCATATCTCAGATGGGCTGATAGATA-TCCCTTGGCAGATCGTACCATC 1813
Db 2223 GCACCTTGTTCATATCTCAGATGGGCTGATAGATA-TCCCTTGGCAGATCGTACCATC 2282
QY 1814 GGTGACAGGGCCATGTAGTAGTCAATTTTGGCCCACTTAGCCCACTGCCTGGAAAGCCCTTC 1873
Db 2283 GGTGACAGGGCCATGTAGTAGTCAATTTTGGCCCACTTAGCCCACTGCCTGGAAAGCCCTTC 2341
QY 1874 GGA 1876
Db 2342 GGA 2344
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RESULT 14
AAT59196

ID AAT59196 standard; cDNA; 2769 BP.

AC AAT59196;

XX AAT59196;

DT 17-JUN-1997 (first entry)

XX Neuronal alpha-bungarotoxin binding protein alpha subunit cDNA.

DE Neuronal alpha-bungarotoxin binding protein alpha 1; cholinergic;

KW ligand binding; ion channel; ss.

XX Gallus sp.

XX Key Location/Qualifiers

FH 71..1513

FT /*tag= a

FT 71..136

FT sig_peptide /*tag= b

FT

mat_peptide 137..1510
/*tag= C

US5599709-A.

04-FEB-1997.

28-SEP-1989; 89US-00413947.

28-SEP-1989; 89US-00413947.

(SALK) SALK INST BIOLOGICAL STUDIES.

Lindstrom JM, Schoepfer RD;

WPI, 1997-118297/11.

P-FSDB; AAW12368.

New isolated neuronal alpha-bungarotoxin-binding protein DNA - used to

screen cholinergic agents and other drugs which may affect ligand

binding, ion channel or other activities of the protein.

Claim 1; Fig 2A-B; 18pp; English.

2 cDNA clones (AAT59196 and AAT59197) respectively code for the alpha1

subunit (AAW12368) and alpha2 subunit (AAW12369) of chick neuronal alpha-

bungarotoxin binding protein (ABBP). They were isolated from an 18-day

embryo chick brain cDNA library using a probe (see also AAT59198) based

on the N-terminal amino acid sequence of chicken brain ABBP. The probe

isolated partial clone pCh29-1, which encoded the N-terminal portion of

alpha1. A subclone, pCh29-3 (ATCC 40641), was used to rescreen the

library, yielding clone pCh31-1 (ATCC 40640), which encoded the entire

alpha2 sequence. A probe based on the C-terminal region of pCh31-1 was

used to obtain clone pCh34-1 (ATCC 40639), encoding the C-terminal portion

of alpha1. The cDNA clones can be used as probes to identify further ABBP

subunits, and in the recombinant prodn. of ABBP

SQ Sequence 2769 BP; 790 A; 604 C; 571 G; 804 T; 0 U; 0 Other;

Query Match 51.1%; Score 958.4; DB 2; Length 2769;

Best Local Similarity 76.8%; Pred. No. 7.2e-199;

Matches 1169; Conservative 1; Mismatches 352; Indels 0; Gaps 0;

QY 61 CCGGAGCTCAACATCGCTGCTCGCGGGAGGCGCTGTGGCTGGCGCTGGCGCGCTGCTC 120

Db 59 CGGCTCCCGGAATGGGCTCCGGCGCTGATGCTGTGGCTGTGGCGCGCGGGCTC 118

QY 121 CTGCAAGTGTCCCTGCAAGGCGAGTTCAGAGGAGCTTTCAAGAGAGCTGGTCAAGAAC 180

Db 119 GTGCGGAGTCCCTGCAAGGAGAGTTCCAAGGAGAGTGTACAAGGAGCTGCTGAAGAAC 178

QY 181 TACAATCCCTGGAGAGGCGCTGCGCAATGACTCGCAACCACTCACCGTCTACTTCTCC 240

Db 179 TACAATCCCTGGAGAGGCGCTGCGCAATGACTCGCAACCACTCACCGTCTACTTCTCC 238

QY 241 CTGAGCCTCTTCAGATCATGAGCGTGGATGAGAGAACCAAGTTTAAACCAACCAATT 300

Db 239 CTCAGCCTCATGAGATCATGATGTGATGAAAGATCAAGTATTAAACCAACCAATC 298

QY 301 TGGCTGCAATGTCTTGGAGAGAGTTCATTTTCAAGTGAATGTGTCAAGATATCCAGGG 360

Db 299 TGGCTGCAATGTCTTGGAGAGAGTTCATTTTCAAGTGAATGTGTCAAGATATCCAGGG 358

QY 361 GTGAAGAGTGTTCCTTCCAGAGTGGCAGATTTTGAAGAGAGAGTTCCTCTCTATTAAC 420

Db 359 GTGAAGAGTGTTCCTTCCAGAGTGGCAGATTTTGAAGAGAGAGTTCCTCTCTATTAAC 418

QY 421 AGTGTGATGAGCGCTTGGAGCGGAGAGTTCACACTAACCGTGTGGTGAATCTTCTGGG 480

Db 419 AGTGTGATGAGCGCTTGGAGCGGAGAGTTCACACTAACCGTGTGGTGAATCTTCTGGG 478

QY 481 CATTGCCAGTACCTGCGCTCCAGGAGATATTCAGAGTTCCTCTCATCGATGTACGCTGG 540

Db

QY

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QY

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[illegible]

RESULT 15
AAC90382

AAC90382
 ID AAC90382 standard; CDNA; 1416 BP.

AAC90382;

XX
XXXXX

DT 11-SEP-2003 (revised)

DT 14-MAR-2001 (first entry)

DE Chimeric alpha7/5-HT3 ligand gated ion channel coding sequence.

XX

KW Murine; alpha7 nicotinic acetylcholine gated ion channel; human;

XX
XXI
XXII

OS Mus musculus.

OS Homo sapi

OS Chimeric.

XX

PN WO200073431-A2.

XX

PD 07-DEC-2000.

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PF 25-MAY-2000; 2000WO-

XX 27 1000

PR 27-MAY-1999; 99US-0136174P.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.

XX

PI Groppi VE, Wolfe ML, Berkenpas MB;

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DR WPI; 2001-061524/07.

DR P-PSDB; AAB50014.
vv

XX special cell culture medium for treating cells and for inducing mammalian

PI special cell culture medium for treating cells and for inducing mammalian cell lines to conduct calcium ions comprising specified concentrations

PT of ions of sodium, calcium and potassium at specified pH.

XX
TO STAY TO
LIVING, AND
THEY WERE
XX

PS Claim 43: Page 66; 77pp; English.

[illegible]

CC The present sequence is the coding sequence for a chimeric human alpha7

CC nicotinic acetylcholine/murine 5-hydroxytryptamine (5-HT3) ligand gated

CC ion channel. The $\alpha 7/5$ -HT3 chimeric ion channel can be expressed by

CC recombinant cells in the present invention, resulting in preferential

```
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Job time : 796 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 15:51:58 ; Search time 7438 Seconds
(without alignments)
10931.908 Million cell updates/sec

Title: US-09-703-951A-11
Perfect score: 1876
Sequence: 1 GGCOCAGGCGCAGGCCCGG.....TGCCTGGAAGCCCTTCGGA 1876

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

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11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_on.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_hg_hum.*

31: em_hg_inv.*

32: em_hg_other.*

33: em_hg_mus.*

34: em_hg_pln.*

35: em_hg_tod.*

36: em_hg_nam.*

37: em_hg_vrt.*

38: em_sy.*

39: em_hgo_hum.*

40: em_hgo_mus.*

41: em_hgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1875.6	100.0	1876	6	AR055255	AR055255 Sequence
2	1875.6	100.0	1876	6	AR071403	AR071403 Sequence
3	1875.6	100.0	1876	6	AR173187	AR173187 Sequence
4	1875.6	100.0	1876	6	AR224030	AR224030 Sequence
5	1875.6	100.0	1876	6	AR282833	AR282833 Sequence
6	1875.6	100.0	1876	6	AX719088	AX719088 Sequence
7	1875.6	100.0	1876	9	HSU62436	U62436 Human nicot
8	1801.2	96.0	1916	9	AF385585	AF385585 Homo sapi
9	1801	96.0	1977	9	HSU40583	U40583 Human alpha
10	1801	96.0	2087	9	HSARA7A	X70297 H.sapiens m
11	1745.2	93.0	2107	9	AF486623	AF486623 Macaca mu
12	1543	82.2	1590	6	AR261850	AR261850 Sequence
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14	1520.4	81.0	1559	9	HUMA7NAR	L25827 Human a7 ni
15	1508.6	80.4	1509	6	AX054567	AX054567 Sequence
16	1507	80.3	1509	6	AX054575	AX054575 Sequence
17	1507	80.3	1509	6	AX054577	AX054577 Sequence
18	1505.4	80.2	1509	6	AX054579	AX054579 Sequence
19	1505.4	80.2	1509	9	HGNACHRA7	Y08420 H.sapiens m
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23	1391.2	74.2	1712	9	AF036903	AF036903 Homo sapi
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26	1217.4	64.9	2106	10	RATNARAD	L31619 Rattus ratt
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41	647	34.5	2090	5	GGANAREC	AY299465 Takifugu
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45	509.8	27.2	1665	5	AY298753	AY298752 Takifugu

ALIGNMENTS

RESULT 1
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LOCUS AR055255 1876 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 7 from patent US 5837489.
ACCESSION AR055255
VERSION AR055255.1 GI:5980832
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1876)
AUTHORS Elliott,K.J., Ellis,S.B. and Harpold,M.M.
TITLE Human neuronal nicotinic acetylcholine receptor and cells
transformed with same DNA and mRNA encoding an--subunit of
JOURNAL Patent: US 5837489-A 7 17-NOV-1998;

FEATURES		Location/Qualifiers
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		/mol_type="unassigned DNA"
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Db	1	GGCCGAGCGCAGGCGCGGCGCAGCGAGACGTGGAGCGCGCGGCTGCGTGCAGCT 60
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Db	61	CGGGGACTCAACATGCGTCTCGCGGAGGCGCTGCGTGCCTGCGCGCGTGCCTC 120
QY	121	CTGACGCTGCTCCGCAAGCGAGTTCAGAGGAAGCTTTCAAGGAGCTGGTCAAGAAC 180
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QY	241	CTGAGCTCTGAGAGTCAAGGAGTGGAGTGAAGAACCAAGTTTAAACCAACAATT 300
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RESULT 2
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LOCUS
DEFINITION Sequence 7 from patent US 5910582.
ACCESSION AR071403
VERSION AR071403.1 GI:7222291
KEYWORDS

linear PAT 18-FEB-2000

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1876)
AUTHORS Elliott, K.J., Ellis, S.B. and Harpold, M.M.
TITLE Human neuronal nicotinic acetylcholine receptor compositions and methods employing same
JOURNAL Patent: US 5910582-A 7 08-JUN-1999;
FEATURES Location/Qualifiers
source 1..1876
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 1875.6; DB 6; Length 1876;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1876; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS ARI173187 1876 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 7 from patent US 6303753.
ACCESSION ARI173187
VERSION ARI173187.1 GI:17912678
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1. (bases 1 to 1876)
AUTHORS Elliott,K.J., Ellis,S.B. and Harpold,M.M.
TITLE Human neuronal nicotinic acetylcholine receptor compositions and
methods employing same
JOURNAL Patent: US 6303753-A 7 16-OCT-2001;
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Best Local Similarity 100.0%; Pred. No. 0;
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LOCUS
DEFINITION Sequence 11 from patent US 6440681.
ACCESSION AR224030
VERSION AR224030.1 GI:23332638
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 1876)
AUTHORS Elliott,K.J.; Ellis,S.B. and Harpold,M.M.
TITLE Methods for identifying agonists and antagonists for human neuronal
nicotinic acetylcholine receptors
JOURNAL Patent: US 6440681-A 11 27-AUG-2002;
FEATURES Location/Qualifiers
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ORIGIN
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LOCUS AR282833 1876 bp DNA linear PAT 10-APR-2003
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ACCESSION AR282833
VERSION AR282833.1 GI:29719625
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 1876)

AUTHORS Elliott, K.J. and Harpold, M.M.

TITLE Human neuronal nicotinic acetylcholine receptor compositions and

METHODS employing same

JOURNAL Patent: US 6524789-A 11 25-FEB-2003;

FEATURES Location/Qualifiers

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REFERENCE 2 (bases 1 to 1977)
AUTHORS Leonard, S.
TITLE Direct Submission
JOURNAL Submitted (13-NOV-1995) Sherry Leonard, University of Colorado
Health Sciences Center, C-268-71 Pharmacology, 4200 E. Ninth Ave,
Denver, CO 80262, USA

FEATURES
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 VERSION X70297.1 GI:496606
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 Peng, X., Katz, M., Gerzanich, V., Anand, R. and Lindstrom, J.
 Human alpha 7 acetylcholine receptor: cloning of the alpha 7 subunit from the SH-SY5y cell line and determination of pharmacological properties of native receptors and functional alpha 7 homomers expressed in Xenopus oocytes
 Mol. Pharmacol. 45 (3), 546-554 (1994)
 94195283
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 2 (bases 1 to 2087)
 Katz, M.
 Direct Submission
 Submitted (04-FEB-1993) M. Katz, Univ of Pennsylvania School of Medicine, Dept of Neuroscience, 36th & Hamilton Walk, Rm 235
 Stemmler Hall, Philadelphia, PA 19104, USA
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RESULT 11
LOCUS AF486623
DEFINITION Macaca mulatta nicotinic acetylcholine receptor alpha7 (CHRNA7)
ACCESSION AF486623

VERSION
KEYWORDS
SOURCE
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gene
5' UTR
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ORIGIN

Query Match
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Matches 1800; Conservative 1; Mismatches 74; Indels 1; Gaps 1;

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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Macaca.
1 (bases 1 to 2107)
Proskocil, B.J., Sekhon, H.S., Kellier, J.A., Jia, Y., Blakely, R.D.,
Lindstrom, J., and Spindel, E.R.
An Intrinsic Non-neuronal Nicotinic Cholinergic Signaling System in
Monkey Lung Airway Epithelium
Unpublished
2 (bases 1 to 2107)
Proskocil, B.J., Sekhon, H.S., Kellier, J.A., Jia, Y., Blakely, R.D.,
Lindstrom, J., and Spindel, E.R.
Direct Submission
Submitted (21-FEB-2002) Neuroscience, Oregon Regional Primate
Research Center, 505 NW 185th Ave., Beaverton, OR 97006, USA
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RESULT 12
AR261850
LOCUS AR261850 1590 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 1 from patent US 6323000.
ACCESSION AR261850
VERSION AR261850.1 GI:28073040
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 1590)
AUTHORS Briggs,C.A., Gopalakrishnan,M., McKenna,D.G., Monteggia,L.M.,
Roch,J.-M., Sullivan,J.P. and Touma,E.
TITLE Variant human .alpha.7 acetylcholine receptor subunit, and methods
of production and uses thereof
JOURNAL Patent: US 6323000-A 1 27-NOV-2001;
FEATURES Location/Qualifiers
source 1..1590
/organism="unknown"
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ORIGIN

Query Match 82.2%; Score 1543; DB 6; Length 1590;
Best Local Similarity 98.6%; Pred. No. 1.3e-270;
Matches 1555; Conservative 1; Mismatches 21; Indels 0; Gaps 0;
72 CATGCGCTGCTCGCGCGGAGCGCTGCGTGGCGCTGGCGCGCTCGCTCGACGTGTC 131
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68 CTGCAAGCGGAGTTCAGAGGAAGCTTTTACAAGAGCTGGTCAAGAACTCAATCCCTT 127
192 GGAGAGGCGCGTGGCCNATGACTCGCAACCACTCAACGCTACTTCTCCCTGAGCTCCT 251
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252 GCAGATCATGGAGCTGGATGAGAAGAACCAAGTTTTTAACCAACCAATTTGGCTGCAAT 311


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RESULT 14
HUMA7NAR
LOCUS 1559 bp mRNA linear PRI 04-JAN-1994
DEFINITION Human a7 nicotinic acetylcholine receptor mRNA.
ACCESSION L25827
VERSION L25827.1 GI:438616
KEYWORDS nicotinic acetylcholine receptor alpha 7 subunit; transmembrane protein.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Doveitte-Stamm, L., Monteggia, L.M., Donnelly-Roberts, D., Wang, M.T., Lee, J., Tian, J. and Giordano, T.
TITLE Cloning and sequence of the human a7 nicotinic acetylcholine receptor
JOURNAL Drug Dev. Res. (1993) In press
COMMENT Original source text: Homo sapiens (library: Clontech HL1065b; ATCC 37433) fetus brain cDNA to mRNA.
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ORIGIN

Query Match 81.0%; Score 1520.4; DB 9; Length 1559;
Best Local Similarity 99.5%; Pred. No. 1.7e-266;
Matches 1524; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

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QY 177 GAATACAAATCCCTTGGAGAGCGCGTGGCCAAATGACTCGCAACCACTTCACCGTCTACTT 236
Db 82 GAATACAAATCCCTTGGAGAGCGCGTGGCCAAATGACTCGCAACCACTTCACCGTCTACTT 141
QY 237 CTCCCTGAGCCTCTGCGAGATCATGGAGTGTGAGAGAACCAAGTTTAAACCAACAA 296
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QY	357	AGGGGTGAAGACTGTTCGTTTCCAGATGGCCAGATTTCGAAACCAGACATTTCTTCTCTA	416
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QY	537	CTGGTTTCCCTTTGANGTGCAGCACTGCACAACTGAAAGTTTGGGTCTCTGGTTCTACGGAGG	596
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QY	597	CTGGTCTCTCGATCTGCAGATGCGAGGCGAGATATCAGTGGCTATATCCCAATGAGAGA	656
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QY	777	CAACCTGCTGATCCCGTGTGCTCATCTCGGCCCTCGCCCTGCTGCTGTCTCGTCTTC	836
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Qy	1437	GGTCTGCAGCGAGTGGAAAGTTTCGCGCGCTGTGTGGTGGACCGCCTGTGCCTCATGGCCTT	1496
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Qy	1497	CTCGGTCTTACCAATCATCTGCACCATCGGCATCCTCATGATTCGGCTCCCAACTTCGTGGGA	1556
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Qy	1557	GGCCGTGTCCAAAGACACTTTCGTAACCAACGCTGGTTCGTACATGTGGAAACTACAG	1616
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LOCUS	AX054567	1509 bp	DNA
DEFINITION	Sequence 1 from Patent WO0073431.		PAT 13-JAN-2001
ACCESSION	AX054567		
VERSION	AX054567.1	GI:12228147	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1		
AUTHORS	Groppi, V.E., Wolfe, M.L. and Berkenpas, M.B.		
TITLE	Methods and compositions for measuring ion channel conductance		
JOURNAL	Patent: WO 0073431-A 1 07-DEC-2000;		
FEATURES	PHARMACIA & UPJOHN COMPANY (US)		
source	Location/Qualifiers		
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Best Local Similarity	99.9%;	Pred. No. 2.4e-264;	
Matches 1508;	Conservative	1;	Mismatches 0;
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Qy	133	CTGCAAGCGCGAGTTCCAGAGGAAGCTTTTCAAGGAGCTGGTCAAGAACTACAATCCCTTG	192
Db	61	CTGCAAGCGCGAGTTCCAGAGGAAGCTTTCAAGGAGCTGGTCAAGAACTACAATCCCTTG	120
Qy	193	GAGAGGCCCTGGCCAATGACTGCAACCACTCACCGTCTATTCTCCCTGAGCCTCCCTG	252
Db	121	GAGAGGCCCTGGCCAATGACTGCAACCACTCACCGTCTATTCTCCCTGAGCCTCCCTG	180
Qy	253	CAGATCATGACCTGGATGAGAAGAACCAAGTTTTTAACCAACCAATTTGGCTGGCAATG	312
Db	181	CAGATCATGACCTGGATGAGAAGAACCAAGTTTTTAACCAACCAATTTGGCTGGCAATG	240
Qy	313	TCTTGGACAGATCACTATTTPACAGTGGAAATGTCTCAGAATATCCAGGGGTGAAGACTGTT	372
Db	241	TCTTGGACAGATCACTATTTPACAGTGGAAATGTCTCAGAATATCCAGGGGTGAAGACTGTT	300
Qy	373	CGTTTCCCGAGTGGCCAGATTGGAAACCAAGCAATTTCTCTATTAACAGTGGTATGAG	432
Db	301	CGTTTCCCGAGTGGCCAGATTGGAAACCAAGCAATTTCTCTATTAACAGTGGTATGAG	360
Qy	433	CGCTTTGACGCCACATTTCCACACTAACGCTGTGGTGAATTTCTCTGGGCATTTGCCAGTAC	492

